

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
3 January 2002 (03.01.2002)

PCT

(10) International Publication Number
WO 02/00174 A2

(51) International Patent Classification⁷: **A61K**

(21) International Application Number: **PCT/US01/21065**

(22) International Filing Date: **28 June 2001 (28.06.2001)**

(25) Filing Language: **English**

(26) Publication Language: **English**

(30) Priority Data:
09/606,421 28 June 2000 (28.06.2000) US
09/630,940 2 August 2000 (02.08.2000) US
09/643,597 21 August 2000 (21.08.2000) US
09/662,786 15 September 2000 (15.09.2000) US
09/685,696 9 October 2000 (09.10.2000) US
09/735,705 12 December 2000 (12.12.2000) US
09/850,716 7 May 2001 (07.05.2001) US

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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CI, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: **COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER**

(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer, are disclosed. Illustrative compositions comprise one or more lung tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly lung cancer.



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COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER

TECHNICAL FIELD OF THE INVENTION

5 The present invention relates generally to therapy and diagnosis of cancer, such as lung cancer. The invention is more specifically related to polypeptides, comprising at least a portion of a lung tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides are useful in pharmaceutical compositions, *e.g.*, vaccines, and other compositions for the diagnosis and treatment of
10 lung cancer.

BACKGROUND OF THE INVENTION

Cancer is a significant health problem throughout the world. Although advances have been made in detection and therapy of cancer, no vaccine or other universally successful method for prevention and/or treatment is currently available.
15 Current therapies, which are generally based on a combination of chemotherapy or surgery and radiation, continue to prove inadequate in many patients.

Lung cancer is the primary cause of cancer death among both men and women in the U.S., with an estimated 172,000 new cases being reported in 1994. The five-year survival rate among all lung cancer patients, regardless of the stage of disease
20 at diagnosis, is only 13%. This contrasts with a five-year survival rate of 46% among cases detected while the disease is still localized. However, only 16% of lung cancers are discovered before the disease has spread.

In spite of considerable research into therapies for these and other cancers, lung cancer remains difficult to diagnose and treat effectively. Accordingly,
25 there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

In one aspect, the present invention provides polynucleotide compositions comprising a sequence selected from the group consisting of:

- (a) sequences provided in SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467;
- (b) complements of the sequences provided in SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467;
- (c) sequences consisting of at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 75 and 100 contiguous residues of a sequence provided in SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467;
- (d) sequences that hybridize to a sequence provided in SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467, under moderate or highly stringent conditions;

(e) sequences having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identity to a sequence of SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467; and

(f) degenerate variants of a sequence provided in SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467.

In one preferred embodiment, the polynucleotide compositions of the invention are expressed in at least about 20%, more preferably in at least about 30%, and most preferably in at least about 50% of lung tumors samples tested, at a level that is at least about 2-fold, preferably at least about 5-fold, and most preferably at least about 10-fold higher than that for normal tissues.

The present invention, in another aspect, provides polypeptide compositions comprising an amino acid sequence that is encoded by a polynucleotide sequence described above.

The present invention further provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NOs:152, 155, 156, 165, 166, 169, 170, 172, 174, 176, 226-252, 338-344, 346, 350, 357, 361, 363, 365, 367, 369, 376-382, 387-419, 423, 427, 430, 433, 441, 443, 446, 449 and 451-466, .

In certain preferred embodiments, the polypeptides and/or polynucleotides of the present invention are immunogenic, *i.e.*, they are capable of eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.

The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the fragments, variants and/or derivatives preferably have a level of immunogenic activity of at least about 50%, preferably at least about 70% and more preferably at least about 5 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID NOs:152, 155, 156, 165, 166, 169, 170, 172, 174, 176, 226-252, 338-344, 346, 350, 357, 361, 363, 365, 367, 369, 376-382, 387-419, 423, 427, 430, 433, 441, 443, 446, 449 and 451-466, or a polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 10 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467.

The present invention further provides polynucleotides that encode a 15 polypeptide described above, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

20 Within a related aspect of the present invention, the pharmaceutical compositions, *e.g.*, vaccine compositions, are provided for prophylactic or therapeutic applications. Such compositions generally comprise an immunogenic polypeptide or polynucleotide of the invention and an immunostimulant, such as an adjuvant.

The present invention further provides pharmaceutical compositions that 25 comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as 30 described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative

antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above
5 and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier and/or an
10 immunostimulant. The fusions proteins may comprise multiple immunogenic polypeptides or portions/variants thereof, as described herein, and may further comprise one or more polypeptide segments for facilitating the expression, purification and/or immunogenicity of the polypeptide(s).

Within further aspects, the present invention provides methods for
15 stimulating an immune response in a patient, preferably a T cell response in a human patient, comprising administering a pharmaceutical composition described herein. The patient may be afflicted with lung cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

20 Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition as recited above. The patient may be afflicted with lung cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

25 The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating
5 and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells
10 prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the
15 development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount
20 of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer, preferably a lung cancer, in a patient
25 comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent
30 is an antibody, more preferably a monoclonal antibody.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount

detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as
5 diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if
10 each was incorporated individually.

SEQUENCE IDENTIFIERS

- SEQ ID NO:1 is the determined cDNA sequence for LST-S1-2
SEQ ID NO:2 is the determined cDNA sequence for LST-S1-28
SEQ ID NO:3 is the determined cDNA sequence for LST-S1-90
15 SEQ ID NO:4 is the determined cDNA sequence for LST-S1-144
SEQ ID NO:5 is the determined cDNA sequence for LST-S1-133
SEQ ID NO:6 is the determined cDNA sequence for LST-S1-169
SEQ ID NO:7 is the determined cDNA sequence for LST-S2-6
SEQ ID NO:8 is the determined cDNA sequence for LST-S2-11
20 SEQ ID NO:9 is the determined cDNA sequence for LST-S2-17
SEQ ID NO:10 is the determined cDNA sequence for LST-S2-25
SEQ ID NO:11 is the determined cDNA sequence for LST-S2-39
SEQ ID NO:12 is a first determined cDNA sequence for LST-S2-43
SEQ ID NO:13 is a second determined cDNA sequence for LST-S2-43
25 SEQ ID NO:14 is the determined cDNA sequence for LST-S2-65
SEQ ID NO:15 is the determined cDNA sequence for LST-S2-68
SEQ ID NO:16 is the determined cDNA sequence for LST-S2-72
SEQ ID NO:17 is the determined cDNA sequence for LST-S2-74
SEQ ID NO:18 is the determined cDNA sequence for LST-S2-103

- SEQ ID NO:19 is the determined cDNA sequence for LST-S2-N1-1F
SEQ ID NO:20 is the determined cDNA sequence for LST-S2-N1-2A
SEQ ID NO:21 is the determined cDNA sequence for LST-S2-N1-4H
SEQ ID NO:22 is the determined cDNA sequence for LST-S2-N1-5A
5 SEQ ID NO:23 is the determined cDNA sequence for LST-S2-N1-6B
SEQ ID NO:24 is the determined cDNA sequence for LST-S2-N1-7B
SEQ ID NO:25 is the determined cDNA sequence for LST-S2-N1-7H
SEQ ID NO:26 is the determined cDNA sequence for LST-S2-N1-8A
SEQ ID NO:27 is the determined cDNA sequence for LST-S2-N1-8D
10 SEQ ID NO:28 is the determined cDNA sequence for LST-S2-N1-9A
SEQ ID NO:29 is the determined cDNA sequence for LST-S2-N1-9E
SEQ ID NO:30 is the determined cDNA sequence for LST-S2-N1-10A
SEQ ID NO:31 is the determined cDNA sequence for LST-S2-N1-10G
SEQ ID NO:32 is the determined cDNA sequence for LST-S2-N1-11A
15 SEQ ID NO:33 is the determined cDNA sequence for LST-S2-N1-12C
SEQ ID NO:34 is the determined cDNA sequence for LST-S2-N1-12E
SEQ ID NO:35 is the determined cDNA sequence for LST-S2-B1-3D
SEQ ID NO:36 is the determined cDNA sequence for LST-S2-B1-6C
SEQ ID NO:37 is the determined cDNA sequence for LST-S2-B1-5D
20 SEQ ID NO:38 is the determined cDNA sequence for LST-S2-B1-5F
SEQ ID NO:39 is the determined cDNA sequence for LST-S2-B1-6G
SEQ ID NO:40 is the determined cDNA sequence for LST-S2-B1-8A
SEQ ID NO:41 is the determined cDNA sequence for LST-S2-B1-8D
SEQ ID NO:42 is the determined cDNA sequence for LST-S2-B1-10A
25 SEQ ID NO:43 is the determined cDNA sequence for LST-S2-B1-9B
SEQ ID NO:44 is the determined cDNA sequence for LST-S2-B1-9F
SEQ ID NO:45 is the determined cDNA sequence for LST-S2-B1-12D
SEQ ID NO:46 is the determined cDNA sequence for LST-S2-I2-2B
SEQ ID NO:47 is the determined cDNA sequence for LST-S2-I2-5F
30 SEQ ID NO:48 is the determined cDNA sequence for LST-S2-I2-6B

- SEQ ID NO:49 is the determined cDNA sequence for LST-S2-I2-7F
SEQ ID NO:50 is the determined cDNA sequence for LST-S2-I2-8G
SEQ ID NO:51 is the determined cDNA sequence for LST-S2-I2-9E
SEQ ID NO:52 is the determined cDNA sequence for LST-S2-I2-12B
5 SEQ ID NO:53 is the determined cDNA sequence for LST-S2-H2-2C
SEQ ID NO:54 is the determined cDNA sequence for LST-S2-H2-1G
SEQ ID NO:55 is the determined cDNA sequence for LST-S2-H2-4G
SEQ ID NO:56 is the determined cDNA sequence for LST-S2-H2-3H
SEQ ID NO:57 is the determined cDNA sequence for LST-S2-H2-5G
10 SEQ ID NO:58 is the determined cDNA sequence for LST-S2-H2-9B
SEQ ID NO:59 is the determined cDNA sequence for LST-S2-H2-10H
SEQ ID NO:60 is the determined cDNA sequence for LST-S2-H2-12D
SEQ ID NO: 61 is the determined cDNA sequence for LST-S3-2
SEQ ID NO: 62 is the determined cDNA sequence for LST-S3-4
15 SEQ ID NO: 63 is the determined cDNA sequence for LST-S3-7
SEQ ID NO: 64 is the determined cDNA sequence for LST-S3-8
SEQ ID NO: 65 is the determined cDNA sequence for LST-S3-12
SEQ ID NO: 66 is the determined cDNA sequence for LST-S3-13
SEQ ID NO: 67 is the determined cDNA sequence for LST-S3-14
20 SEQ ID NO: 68 is the determined cDNA sequence for LST-S3-16
SEQ ID NO: 69 is the determined cDNA sequence for LST-S3-21
SEQ ID NO: 70 is the determined cDNA sequence for LST-S3-22
SEQ ID NO: 71 is the determined cDNA sequence for LST-S1-7
SEQ ID NO: 72 is the determined cDNA sequence for LST-S1-A-1E
25 SEQ ID NO: 73 is the determined cDNA sequence for LST-S1-A-1G
SEQ ID NO: 74 is the determined cDNA sequence for LST-S1-A-3E
SEQ ID NO: 75 is the determined cDNA sequence for LST-S1-A-4E
SEQ ID NO: 76 is the determined cDNA sequence for LST-S1-A-6D
SEQ ID NO: 77 is the determined cDNA sequence for LST-S1-A-8D
30 SEQ ID NO: 78 is the determined cDNA sequence for LST-S1-A-10A

- SEQ ID NO: 79 is the determined cDNA sequence for LST-S1-A-10C
SEQ ID NO: 80 is the determined cDNA sequence for LST-S1-A-9D
SEQ ID NO: 81 is the determined cDNA sequence for LST-S1-A-10D
SEQ ID NO: 82 is the determined cDNA sequence for LST-S1-A-9H
5 SEQ ID NO: 83 is the determined cDNA sequence for LST-S1-A-11D
SEQ ID NO: 84 is the determined cDNA sequence for LST-S1-A-12D
SEQ ID NO: 85 is the determined cDNA sequence for LST-S1-A-11E
SEQ ID NO: 86 is the determined cDNA sequence for LST-S1-A-12E
SEQ ID NO: 87 is the determined cDNA sequence for L513S (T3).
10 SEQ ID NO: 88 is the determined cDNA sequence for L513S contig 1.
SEQ ID NO: 89 is a first determined cDNA sequence for L514S.
SEQ ID NO: 90 is a second determined cDNA sequence for L514S.
SEQ ID NO: 91 is a first determined cDNA sequence for L516S.
SEQ ID NO: 92 is a second determined cDNA sequence for L516S.
15 SEQ ID NO: 93 is the determined cDNA sequence for L517S.
SEQ ID NO: 94 is the extended cDNA sequence for LST-S1-169 (also known as L519S).
SEQ ID NO: 95 is a first determined cDNA sequence for L520S.
SEQ ID NO: 96 is a second determined cDNA sequence for L520S.
20 SEQ ID NO: 97 is a first determined cDNA sequence for L521S.
SEQ ID NO: 98 is a second determined cDNA sequence for L521S.
SEQ ID NO: 99 is the determined cDNA sequence for L522S.
SEQ ID NO: 100 is the determined cDNA sequence for L523S.
SEQ ID NO: 101 is the determined cDNA sequence for L524S.
25 SEQ ID NO: 102 is the determined cDNA sequence for L525S.
SEQ ID NO: 103 is the determined cDNA sequence for L526S.
SEQ ID NO: 104 is the determined cDNA sequence for L527S.
SEQ ID NO: 105 is the determined cDNA sequence for L528S.
SEQ ID NO: 106 is the determined cDNA sequence for L529S.
30 SEQ ID NO: 107 is a first determined cDNA sequence for L530S.

- SEQ ID NO: 108 is a second determined cDNA sequence for L530S.
- SEQ ID NO: 109 is the determined full-length cDNA sequence for L531S short form
- SEQ ID NO: 110 is the amino acid sequence encoded by SEQ ID NO: 109.
- SEQ ID NO: 111 is the determined full-length cDNA sequence for L531S long form
- 5 SEQ ID NO: 112 is the amino acid sequence encoded by SEQ ID NO: 111.
- SEQ ID NO: 113 is the determined full-length cDNA sequence for L520S.
- SEQ ID NO: 114 is the amino acid sequence encoded by SEQ ID NO: 113.
- SEQ ID NO: 115 is the determined cDNA sequence for contig 1.
- SEQ ID NO: 116 is the determined cDNA sequence for contig 3.
- 10 SEQ ID NO: 117 is the determined cDNA sequence for contig 4.
- SEQ ID NO: 118 is the determined cDNA sequence for contig 5.
- SEQ ID NO: 119 is the determined cDNA sequence for contig 7.
- SEQ ID NO: 120 is the determined cDNA sequence for contig 8.
- SEQ ID NO: 121 is the determined cDNA sequence for contig 9.
- 15 SEQ ID NO: 122 is the determined cDNA sequence for contig 10.
- SEQ ID NO: 123 is the determined cDNA sequence for contig 12.
- SEQ ID NO: 124 is the determined cDNA sequence for contig 11.
- SEQ ID NO: 125 is the determined cDNA sequence for contig 13 (also known as L761P).
- 20 SEQ ID NO: 126 is the determined cDNA sequence for contig 15.
- SEQ ID NO: 127 is the determined cDNA sequence for contig 16.
- SEQ ID NO: 128 is the determined cDNA sequence for contig 17.
- SEQ ID NO: 129 is the determined cDNA sequence for contig 19.
- SEQ ID NO: 130 is the determined cDNA sequence for contig 20.
- 25 SEQ ID NO: 131 is the determined cDNA sequence for contig 22.
- SEQ ID NO: 132 is the determined cDNA sequence for contig 24.
- SEQ ID NO: 133 is the determined cDNA sequence for contig 29.
- SEQ ID NO: 134 is the determined cDNA sequence for contig 31.
- SEQ ID NO: 135 is the determined cDNA sequence for contig 33.
- 30 SEQ ID NO: 136 is the determined cDNA sequence for contig 38.

- SEQ ID NO: 137 is the determined cDNA sequence for contig 39.
SEQ ID NO: 138 is the determined cDNA sequence for contig 41.
SEQ ID NO: 139 is the determined cDNA sequence for contig 43.
SEQ ID NO: 140 is the determined cDNA sequence for contig 44.
5 SEQ ID NO: 141 is the determined cDNA sequence for contig 45.
SEQ ID NO: 142 is the determined cDNA sequence for contig 47.
SEQ ID NO: 143 is the determined cDNA sequence for contig 48.
SEQ ID NO: 144 is the determined cDNA sequence for contig 49.
SEQ ID NO: 145 is the determined cDNA sequence for contig 50.
10 SEQ ID NO: 146 is the determined cDNA sequence for contig 53.
SEQ ID NO: 147 is the determined cDNA sequence for contig 54.
SEQ ID NO: 148 is the determined cDNA sequence for contig 56.
SEQ ID NO: 149 is the determined cDNA sequence for contig 57.
SEQ ID NO: 150 is the determined cDNA sequence for contig 58.
15 SEQ ID NO: 151 is the full-length cDNA sequence for L530S.
SEQ ID NO: 152 is the amino acid sequence encoded by SEQ ID NO: 151
SEQ ID NO: 153 is the full-length cDNA sequence of a first variant of L514S
SEQ ID NO: 154 is the full-length cDNA sequence of a second variant of L514S
SEQ ID NO: 155 is the amino acid sequence encoded by SEQ ID NO: 153.
20 SEQ ID NO: 156 is the amino acid sequence encoded by SEQ ID NO: 154.
SEQ ID NO: 157 is the determined cDNA sequence for contig 59.
SEQ ID NO: 158 is the full-length cDNA sequence for L763P (also referred to as contig 22).
SEQ ID NO: 159 is the amino acid sequence encoded by SEQ ID NO: 158.
25 SEQ ID NO: 160 is the full-length cDNA sequence for L762P (also referred to as contig 17).
SEQ ID NO: 161 is the amino acid sequence encoded by SEQ ID NO: 160.
SEQ ID NO: 162 is the determined cDNA sequence for L515S.
SEQ ID NO: 163 is the full-length cDNA sequence of a first variant of L524S.
30 SEQ ID NO: 164 is the full-length cDNA sequence of a second variant of L524S.

- SEQ ID NO: 165 is the amino acid sequence encoded by SEQ ID NO: 163.
SEQ ID NO: 166 is the amino acid sequence encoded by SEQ ID NO: 164.
SEQ ID NO: 167 is the full-length cDNA sequence of a first variant of L762P.
SEQ ID NO: 168 is the full-length cDNA sequence of a second variant of L762P.
- 5 SEQ ID NO: 169 is the amino acid sequence encoded by SEQ ID NO: 167.
SEQ ID NO: 170 is the amino acid sequence encoded by SEQ ID NO: 168.
SEQ ID NO: 171 is the full-length cDNA sequence for L773P (also referred to as contig 56).
SEQ ID NO: 172 is the amino acid sequence encoded by SEQ ID NO: 171.
- 10 SEQ ID NO: 173 is an extended cDNA sequence for L519S.
SEQ ID NO: 174 is the amino acid sequence encoded by SEQ ID NO: 174.
SEQ ID NO: 175 is the full-length cDNA sequence for L523S.
SEQ ID NO: 176 is the amino acid sequence encoded by SEQ ID NO: 175.
SEQ ID NO: 177 is the determined cDNA sequence for LST-sub5-7A.
- 15 SEQ ID NO: 178 is the determined cDNA sequence for LST-sub5-8G.
SEQ ID NO: 179 is the determined cDNA sequence for LST-sub5-8H.
SEQ ID NO: 180 is the determined cDNA sequence for LST-sub5-10B.
SEQ ID NO: 181 is the determined cDNA sequence for LST-sub5-10H.
SEQ ID NO: 182 is the determined cDNA sequence for LST-sub5-12B.
- 20 SEQ ID NO: 183 is the determined cDNA sequence for LST-sub5-11C.
SEQ ID NO: 184 is the determined cDNA sequence for LST-sub6-1c.
SEQ ID NO: 185 is the determined cDNA sequence for LST-sub6-2f.
SEQ ID NO: 186 is the determined cDNA sequence for LST-sub6-2G.
SEQ ID NO: 187 is the determined cDNA sequence for LST-sub6-4d.
- 25 SEQ ID NO: 188 is the determined cDNA sequence for LST-sub6-4e.
SEQ ID NO: 189 is the determined cDNA sequence for LST-sub6-4f.
SEQ ID NO: 190 is the determined cDNA sequence for LST-sub6-3h.
SEQ ID NO: 191 is the determined cDNA sequence for LST-sub6-5d.
SEQ ID NO: 192 is the determined cDNA sequence for LST-sub6-5h.
- 30 SEQ ID NO: 193 is the determined cDNA sequence for LST-sub6-6h.

- SEQ ID NO: 194 is the determined cDNA sequence for LST-sub6-7a.
SEQ ID NO: 195 is the determined cDNA sequence for LST-sub6-8a.
SEQ ID NO: 196 is the determined cDNA sequence for LST-sub6-7d.
SEQ ID NO: 197 is the determined cDNA sequence for LST-sub6-7e.
5 SEQ ID NO: 198 is the determined cDNA sequence for LST-sub6-8e.
SEQ ID NO: 199 is the determined cDNA sequence for LST-sub6-7g.
SEQ ID NO: 200 is the determined cDNA sequence for LST-sub6-9f.
SEQ ID NO: 201 is the determined cDNA sequence for LST-sub6-9h.
SEQ ID NO: 202 is the determined cDNA sequence for LST-sub6-11b.
10 SEQ ID NO: 203 is the determined cDNA sequence for LST-sub6-11c.
SEQ ID NO: 204 is the determined cDNA sequence for LST-sub6-12c.
SEQ ID NO: 205 is the determined cDNA sequence for LST-sub6-12e.
SEQ ID NO: 206 is the determined cDNA sequence for LST-sub6-12f.
SEQ ID NO: 207 is the determined cDNA sequence for LST-sub6-11g.
15 SEQ ID NO: 208 is the determined cDNA sequence for LST-sub6-12g.
SEQ ID NO: 209 is the determined cDNA sequence for LST-sub6-12h.
SEQ ID NO: 210 is the determined cDNA sequence for LST-sub6-II-1a.
SEQ ID NO: 211 is the determined cDNA sequence for LST-sub6-II-2b.
SEQ ID NO: 212 is the determined cDNA sequence for LST-sub6-II-2g.
20 SEQ ID NO: 213 is the determined cDNA sequence for LST-sub6-II-1h.
SEQ ID NO: 214 is the determined cDNA sequence for LST-sub6-II-4a.
SEQ ID NO: 215 is the determined cDNA sequence for LST-sub6-II-4b.
SEQ ID NO: 216 is the determined cDNA sequence for LST-sub6-II-3e.
SEQ ID NO: 217 is the determined cDNA sequence for LST-sub6-II-4f.
25 SEQ ID NO: 218 is the determined cDNA sequence for LST-sub6-II-4g.
SEQ ID NO: 219 is the determined cDNA sequence for LST-sub6-II-4h.
SEQ ID NO: 220 is the determined cDNA sequence for LST-sub6-II-5c.
SEQ ID NO: 221 is the determined cDNA sequence for LST-sub6-II-5e.
SEQ ID NO: 222 is the determined cDNA sequence for LST-sub6-II-6f.
30 SEQ ID NO: 223 is the determined cDNA sequence for LST-sub6-II-5g.

- SEQ ID NO: 224 is the determined cDNA sequence for LST-sub6-II-6g.
SEQ ID NO: 225 is the amino acid sequence for L528S.
SEQ ID NO: 226-251 are synthetic peptides derived from L762P.
SEQ ID NO: 252 is the expressed amino acid sequence of L514S.
- 5 SEQ ID NO: 253 is the DNA sequence corresponding to SEQ ID NO: 252.
SEQ ID NO: 254 is the DNA sequence of a L762P expression construct.
SEQ ID NO: 255 is the determined cDNA sequence for clone 23785.
SEQ ID NO: 256 is the determined cDNA sequence for clone 23786.
SEQ ID NO: 257 is the determined cDNA sequence for clone 23788.
- 10 SEQ ID NO: 258 is the determined cDNA sequence for clone 23790.
SEQ ID NO: 259 is the determined cDNA sequence for clone 23793.
SEQ ID NO: 260 is the determined cDNA sequence for clone 23794.
SEQ ID NO: 261 is the determined cDNA sequence for clone 23795.
SEQ ID NO: 262 is the determined cDNA sequence for clone 23796.
- 15 SEQ ID NO: 263 is the determined cDNA sequence for clone 23797.
SEQ ID NO: 264 is the determined cDNA sequence for clone 23798.
SEQ ID NO: 265 is the determined cDNA sequence for clone 23799.
SEQ ID NO: 266 is the determined cDNA sequence for clone 23800.
SEQ ID NO: 267 is the determined cDNA sequence for clone 23802.
- 20 SEQ ID NO: 268 is the determined cDNA sequence for clone 23803.
SEQ ID NO: 269 is the determined cDNA sequence for clone 23804.
SEQ ID NO: 270 is the determined cDNA sequence for clone 23805.
SEQ ID NO: 271 is the determined cDNA sequence for clone 23806.
SEQ ID NO: 272 is the determined cDNA sequence for clone 23807.
- 25 SEQ ID NO: 273 is the determined cDNA sequence for clone 23808.
SEQ ID NO: 274 is the determined cDNA sequence for clone 23809.
SEQ ID NO: 275 is the determined cDNA sequence for clone 23810.
SEQ ID NO: 276 is the determined cDNA sequence for clone 23811.
SEQ ID NO: 277 is the determined cDNA sequence for clone 23812.
- 30 SEQ ID NO: 278 is the determined cDNA sequence for clone 23813.

- SEQ ID NO: 279 is the determined cDNA sequence for clone 23815.
SEQ ID NO: 280 is the determined cDNA sequence for clone 25298.
SEQ ID NO: 281 is the determined cDNA sequence for clone 25299.
SEQ ID NO: 282 is the determined cDNA sequence for clone 25300.
5 SEQ ID NO: 283 is the determined cDNA sequence for clone 25301
SEQ ID NO: 284 is the determined cDNA sequence for clone 25304
SEQ ID NO: 285 is the determined cDNA sequence for clone 25309.
SEQ ID NO: 286 is the determined cDNA sequence for clone 25312.
SEQ ID NO: 287 is the determined cDNA sequence for clone 25317.
10 SEQ ID NO:288 is the determined cDNA sequence for clone 25321.
SEQ ID NO:289 is the determined cDNA sequence for clone 25323.
SEQ ID NO:290 is the determined cDNA sequence for clone 25327.
SEQ ID NO:291 is the determined cDNA sequence for clone 25328.
SEQ ID NO:292 is the determined cDNA sequence for clone 25332.
15 SEQ ID NO:293 is the determined cDNA sequence for clone 25333.
SEQ ID NO:294 is the determined cDNA sequence for clone 25336.
SEQ ID NO:295 is the determined cDNA sequence for clone 25340.
SEQ ID NO:296 is the determined cDNA sequence for clone 25342.
SEQ ID NO:297 is the determined cDNA sequence for clone 25356.
20 SEQ ID NO:298 is the determined cDNA sequence for clone 25357.
SEQ ID NO:299 is the determined cDNA sequence for clone 25361.
SEQ ID NO:300 is the determined cDNA sequence for clone 25363.
SEQ ID NO:301 is the determined cDNA sequence for clone 25397.
SEQ ID NO:302 is the determined cDNA sequence for clone 25402.
25 SEQ ID NO:303 is the determined cDNA sequence for clone 25403.
SEQ ID NO:304 is the determined cDNA sequence for clone 25405.
SEQ ID NO:305 is the determined cDNA sequence for clone 25407.
SEQ ID NO:306 is the determined cDNA sequence for clone 25409.
SEQ ID NO:307 is the determined cDNA sequence for clone 25396.
30 SEQ ID NO:308 is the determined cDNA sequence for clone 25414.

- SEQ ID NO:309 is the determined cDNA sequence for clone 25410.
SEQ ID NO:310 is the determined cDNA sequence for clone 25406.
SEQ ID NO:311 is the determined cDNA sequence for clone 25306.
SEQ ID NO:312 is the determined cDNA sequence for clone 25362.
5 SEQ ID NO:313 is the determined cDNA sequence for clone 25360.
SEQ ID NO:314 is the determined cDNA sequence for clone 25398.
SEQ ID NO:315 is the determined cDNA sequence for clone 25355.
SEQ ID NO:316 is the determined cDNA sequence for clone 25351.
SEQ ID NO:317 is the determined cDNA sequence for clone 25331.
10 SEQ ID NO:318 is the determined cDNA sequence for clone 25338.
SEQ ID NO:319 is the determined cDNA sequence for clone 25335.
SEQ ID NO:320 is the determined cDNA sequence for clone 25329.
SEQ ID NO:321 is the determined cDNA sequence for clone 25324.
SEQ ID NO:322 is the determined cDNA sequence for clone 25322.
15 SEQ ID NO:323 is the determined cDNA sequence for clone 25319.
SEQ ID NO:324 is the determined cDNA sequence for clone 25316.
SEQ ID NO:325 is the determined cDNA sequence for clone 25311.
SEQ ID NO:326 is the determined cDNA sequence for clone 25310.
SEQ ID NO:327 is the determined cDNA sequence for clone 25302.
20 SEQ ID NO:328 is the determined cDNA sequence for clone 25315.
SEQ ID NO:329 is the determined cDNA sequence for clone 25308.
SEQ ID NO:330 is the determined cDNA sequence for clone 25303.
SEQ ID NOs:331-337 are the cDNA sequences of isoforms of the p53 tumor suppressor
homologue, p63 (also referred to as L530S).
25 SEQ ID NOs:338-344 are the amino acid sequences encoded by SEQ ID NOs:331-337,
respectively
SEQ ID NO:345 is a second cDNA sequence for the antigen L763P.
SEQ ID NO:346 is the amino acid sequence encoded by the sequence of SEQ ID NO:
345.
30 SEQ ID NO:347 is a determined full-length cDNA sequence for L523S.

- SEQ ID NO:348 is the amino acid sequence encoded by SEQ ID NO: 347.
- SEQ ID NO:349 is the cDNA sequence encoding the N-terminal portion of L773P.
- SEQ ID NO:350 is the amino acid sequence of the N-terminal portion of L773P.
- SEQ ID NO:351 is the DNA sequence for a fusion of Ra12 and the N-terminal portion
5 of L763P
- SEQ ID NO:352 is the amino acid sequence of the fusion of Ra12 and the N-terminal portion of L763P
- SEQ ID NO:353 is the DNA sequence for a fusion of Ra12 and the C-terminal portion of L763P
- 10 SEQ ID NO:354 is the amino acid sequence of the fusion of Ra12 and the C-terminal portion of L763P
- SEQ ID NO:355 is a primer.
- SEQ ID NO:356 is a primer.
- SEQ ID NO:357 is the protein sequence of expressed recombinant L762P.
- 15 SEQ ID NO:358 is the DNA sequence of expressed recombinant L762P.
- SEQ ID NO:359 is a primer.
- SEQ ID NO:360 is a primer.
- SEQ ID NO:361 is the protein sequence of expressed recombinant L773P A.
- SEQ ID NO:362 is the DNA sequence of expressed recombinant L773P A.
- 20 SEQ ID NO:363 is an epitope derived from clone L773P polypeptide.
- SEQ ID NO:364 is a polynucleotide encoding the polypeptide of SEQ ID NO:363.
- SEQ ID NO:365 is an epitope derived from clone L773P polypeptide.
- SEQ ID NO:366 is a polynucleotide encoding the polypeptide of SEQ ID NO:365.
- SEQ ID NO:367 is an epitope consisting of amino acids 571-590 of SEQ ID NO:161,
25 clone L762P.
- SEQ ID NO:368 is the full-length DNA sequence for contig 13 (SEQ ID NO:125), also referred to as L761P.
- SEQ ID NO:369 is the protein sequence encoded by the DNA sequence of SEQ ID NO:368.
- 30 SEQ ID NO:370 is an L762P DNA sequence from nucleotides 2071-2130.

- SEQ ID NO:371 is an L762P DNA sequence from nucleotides 1441-1500.
- SEQ ID NO:372 is an L762P DNA sequence from nucleotides 1936-1955.
- SEQ ID NO:373 is an L762P DNA sequence from nucleotides 2620-2679.
- SEQ ID NO:374 is an L762P DNA sequence from nucleotides 1801-1860.
- 5 SEQ ID NO:375 is an L762P DNA sequence from nucleotides 1531-1591.
- SEQ ID NO:376 is the amino acid sequence of the L762P peptide encoded by SEQ ID NO:373.
- SEQ ID NO:377 is the amino acid sequence of the L762P peptide encoded by SEQ ID NO:370.
- 10 SEQ ID NO:378 is the amino acid sequence of the L762P peptide encoded by SEQ ID NO:372.
- SEQ ID NO:379 is the amino acid sequence of the L762P peptide encoded by SEQ ID NO:374.
- SEQ ID NO:380 is the amino acid sequence of the L762P peptide encoded by SEQ ID
- 15 NO:371.
- SEQ ID NO:381 is the amino acid sequence of the L762P peptide encoded by SEQ ID NO:375.
- SEQ ID NO:382 is the amino acid sequence of an epitope of L762P.
- SEQ ID NOs:383-386 are PCR primers.
- 20 SEQ ID NOs:387-395 are the amino acid sequences of L773P peptides.
- SEQ ID NOs:396-419 are the amino acid sequences of L523S peptides.
- SEQ ID NO:420 is the determined cDNA sequence for clone #19014.
- SEQ ID NO:421 is the forward primer PDM-278 for the L514S-13160 coding region.
- SEQ ID NO:422 is the reverse primer PDM-278 for the L514S-13160 coding region.
- 25 SEQ ID NO:423 is the amino acid sequence for the expressed recombinant L514S.
- SEQ ID NO:424 is the DNA coding sequence for the recombinant L514S.
- SEQ ID NO:425 is the forward primer PDM-414 for the L523S coding region.
- SEQ ID NO:426 is the reverse primer PDM-414 for the L523S coding region.
- SEQ ID NO:427 is the amino acid sequence for the expressed recombinant L523S.
- 30 SEQ ID NO:428 is the DNA coding sequence for the recombinant L523S.

- SEQ ID NO:429 is the reverse primer PDM-279 for the L762PA coding region.
- SEQ ID NO:430 is the amino acid sequence for the expressed recombinant L762PA.
- SEQ ID NO:431 is the DNA coding sequence for the recombinant L762PA.
- SEQ ID NO:432 is the reverse primer PDM-300 for the L773P coding region.
- 5 SEQ ID NO:433 is the amino acid sequence of the expressed recombinant L773P.
- SEQ ID NO:434 is the DNA coding sequence for the recombinant L773P.
- SEQ ID NO:435 is the forward primer for TCR Valpha8.
- SEQ ID NO:436 is the reverse primer for TCR Valpha8.
- SEQ ID NO:437 is the forward primer for TCR Vbeta8.
- 10 SEQ ID NO:438 is the reverse primer for TCR Vbeta8.
- SEQ ID NO:439 is the TCR Valpha DNA sequence of the TCR clone specific for the lung antigen L762P.
- SEQ ID NO:440 is the TCR Vbeta DNA sequence of the TCR clone specific for the lung antigen L762P.
- 15 SEQ ID NO:441 is the amino acid sequence of L763 peptide #2684.
- SEQ ID NO:442 is the predicted full-length cDNA for the cloned partial sequence of clone L529S (SEQ ID NO:106).
- SEQ ID NO:443 is the deduced amino acid sequence encoded by SEQ ID NO:442
- SEQ ID NO:444 is the forward primer PDM-734 for the coding region of clone L523S.
- 20 SEQ ID NO:445 is the reverse primer PDM-735 for the coding region of clone L523S.
- SEQ ID NO:446 is the amino acid sequence for the expressed recombinant L523S.
- SEQ ID NO:447 is the DNA coding sequence for the recombinant L523S.
- SEQ ID NO:448 is another forward primer PDM-733 for the coding region of clone L523S.
- 25 SEQ ID NO:449 is the amino acid sequence for a second expressed recombinant L523S.
- SEQ ID NO:450 is the DNA coding sequence for a second recombinant L523S.
- SEQ ID NO:451 corresponds to amino acids 86-110, an epitope of L514S-specific in the generation of antibodies.
- SEQ ID NO:452 corresponds to amino acids 21-45, an epitope of L514S-specific in the
- 30 generation of antibodies.

- SEQ ID NO:453 corresponds to amino acids 121-135, an epitope of L514S-specific in the generation of antibodies.
- SEQ ID NO:454 corresponds to amino acids 440-460, an epitope of L523S-specific in the generation of antibodies.
- 5 SEQ ID NO:455 corresponds to amino acids 156-175, an epitope of L523S-specific in the generation of antibodies.
- SEQ ID NO:456 corresponds to amino acids 326-345, an epitope of L523S-specific in the generation of antibodies.
- SEQ ID NO:457 corresponds to amino acids 40-59, an epitope of L523S-specific in the
10 generation of antibodies.
- SEQ ID NO:458 corresponds to amino acids 80-99, an epitope of L523S-specific in the generation of antibodies.
- SEQ ID NO:459 corresponds to amino acids 160-179, an epitope of L523S-specific in the generation of antibodies.
- 15 SEQ ID NO:460 corresponds to amino acids 180-199, an epitope of L523S-specific in the generation of antibodies.
- SEQ ID NO:461 corresponds to amino acids 320-339, an epitope of L523S-specific in the generation of antibodies.
- SEQ ID NO:462 corresponds to amino acids 340-359, an epitope of L523S-specific in
20 the generation of antibodies.
- SEQ ID NO:463 corresponds to amino acids 370-389, an epitope of L523S-specific in the generation of antibodies.
- SEQ ID NO:464 corresponds to amino acids 380-399, an epitope of L523S-specific in the generation of antibodies.
- 25 SEQ ID NO:465 corresponds to amino acids 37-55, an epitope of L523S-recognized by the L523S-specific CTL line 6B1.
- SEQ ID NO:466 corresponds to amino acids 41-51, the mapped antigenic epitope of L523S-recognized by the L523S-specific CTL line 6B1.
- SEQ ID NO:467 corresponds to the DNA sequence which encodes SEQ ID NO:466.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed generally to compositions and their use in the therapy and diagnosis of cancer, particularly lung cancer. As described further below, illustrative compositions of the present invention include, but are not restricted to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such polypeptides, antibodies and other binding agents, antigen presenting cells (APCs) and immune system cells (*e.g.*, T cells).

The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook, et al. *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); Maniatis et al. *Molecular Cloning: A Laboratory Manual* (1982); *DNA Cloning: A Practical Approach*, vol. I & II (D. Glover, ed.); *Oligonucleotide Synthesis* (N. Gait, ed., 1984); *Nucleic Acid Hybridization* (B. Hames & S. Higgins, eds., 1985); *Transcription and Translation* (B. Hames & S. Higgins, eds., 1984); *Animal Cell Culture* (R. Freshney, ed., 1986); Perbal, *A Practical Guide to Molecular Cloning* (1984).

All publications, patents and patent applications cited herein, whether *supra* or *infra*, are hereby incorporated by reference in their entirety.

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates otherwise.

25 Polypeptide Compositions

As used herein, the term "polypeptide" is used in its conventional meaning, *i.e.*, as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included

within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both
5 naturally occurring and non-naturally occurring. A polypeptide may be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising epitopes, i.e., antigenic determinants substantially responsible for the immunogenic properties of a polypeptide and being capable of evoking an immune response.

10 Particularly illustrative polypeptides of the present invention comprise those encoded by a polynucleotide sequence set forth in any one of SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209,
15 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly stringent conditions, to a polynucleotide sequence set forth in any one of SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-
20 109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467. Certain illustrative polypeptides of the invention comprise amino acid sequences as set forth in any one of SEQ ID NOs:152, 155, 156,
25 165, 166, 169, 170, 172, 174, 176, 226-252, 338-344, 346, 350, 357, 361, 363, 365, 367, 369, 376-382, 387-419, 423, 427, 430, 433, 441, 443, 446, 449 and 451-466.

The polypeptides of the present invention are sometimes herein referred to as lung tumor proteins or lung tumor polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in
30 lung tumor samples. Thus, a "lung tumor polypeptide" or "lung tumor protein," refers

generally to a polypeptide sequence of the present invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed in a substantial proportion of lung tumor samples, for example preferably greater than about 20%, more preferably greater than about 30%, and most preferably greater than about 50% or more of lung tumor samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in normal tissues, as determined using a representative assay provided herein. A lung tumor polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

In certain preferred embodiments, the polypeptides of the invention are immunogenic, *i.e.*, they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with lung cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one illustrative example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (*i.e.*, specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide. Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they

specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well-known techniques.

In one preferred embodiment, an immunogenic portion of a polypeptide
5 of the present invention is a portion that reacts with antisera and/or T-cells at a level that is not substantially less than the reactivity of the full-length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length
10 polypeptide. In some instances, preferred immunogenic portions will be identified that have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, *e.g.*, having greater than about 100% or 150% or more immunogenic activity.

In certain other embodiments, illustrative immunogenic portions may
15 include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other illustrative immunogenic portions will contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

In another embodiment, a polypeptide composition of the invention may
20 also comprise one or more polypeptides that are immunologically reactive with T cells and/or antibodies generated against a polypeptide of the invention, particularly a polypeptide having an amino acid sequence disclosed herein, or to an immunogenic fragment or variant thereof.

In another embodiment of the invention, polypeptides are provided that
25 comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies that are immunologically reactive with one or more polypeptides described herein, or one or more polypeptides encoded by contiguous nucleic acid sequences contained in the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of
30 these sequences under conditions of moderate to high stringency.

The present invention, in another aspect, provides polypeptide fragments comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide compositions set forth herein, such as those set forth in SEQ ID NOs:152, 155, 156, 165, 166, 169, 170, 172, 174, 176, 226-252, 338-344, 346, 350, 357, 361, 363, 365, 367, 369, 376-382 and 387-419, 441, 443, 446, 449 and 451-466, or those encoded by a polynucleotide sequence set forth in a sequence of SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467.

In another aspect, the present invention provides variants of the polypeptide compositions described herein. Polypeptide variants generally encompassed by the present invention will typically exhibit at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity (determined as described below), along its length, to a polypeptide sequences set forth herein.

In one preferred embodiment, the polypeptide fragments and variants provide by the present invention are immunologically reactive with an antibody and/or T-cell that reacts with a full-length polypeptide specifically set forth herein.

In another preferred embodiment, the polypeptide fragments and variants provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or more of that exhibited by a full-length polypeptide sequence specifically set forth herein.

A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants may be naturally occurring or may be synthetically generated, for example, by modifying one or more of the above polypeptide sequences of the invention and evaluating their immunogenic

activity as described herein and/or using any of a number of techniques well known in the art.

For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader
5 sequence or transmembrane domain, have been removed. Other illustrative variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

In many instances, a variant will contain conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another
10 amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide
15 with desirable characteristics, *e.g.*, with immunogenic characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

20 For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence
25 substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

30

TABLE 1

Amino Acids			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its

hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (−0.4); threonine (−0.7); serine (−0.8); tryptophan (−0.9); tyrosine (−1.3); proline (−1.6); histidine (−3.2); glutamate (−3.5);
5 glutamine (−3.5); aspartate (−3.5); asparagine (−3.5); lysine (−3.9); and arginine (−4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are
10 within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of
15 its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 \pm 1); glutamate (+3.0 \pm 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (−0.4); proline (−0.5 \pm 1); alanine (−0.5); histidine (−0.5); cysteine
20 (−1.0); methionine (−1.3); valine (−1.5); leucine (−1.8); isoleucine (−1.8); tyrosine (−2.3); phenylalanine (−2.5); tryptophan (−3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ± 2
25 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that
30 take various of the foregoing characteristics into consideration are well known to those

of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of
5 flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

10 Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values
15 include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain non-conservative changes. In a
20 preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

25 As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For
30 example, a polypeptide may be conjugated to an immunoglobulin Fc region.

When comparing polypeptide sequences, two sequences are said to be “identical” if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison
5 window to identify and compare local regions of sequence similarity. A “comparison window” as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

10 Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships.
15 In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson,
20 E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be
25 conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics

Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

In one preferred approach, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Within other illustrative embodiments, a polypeptide may be a fusion polypeptide that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known

tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological
5 and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

Fusion polypeptides may generally be prepared using standard
10 techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one
15 polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and
20 second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion polypeptide using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a
25 secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as
30 linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al.,

Proc. Natl. Acad. Sci. USA 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to
5 separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and
10 transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein capable of eliciting a recall response. Examples of such proteins include tetanus,
15 tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

In one preferred embodiment, the immunological fusion partner is derived from a *Mycobacterium* sp., such as a *Mycobacterium tuberculosis*-derived Ra12 fragment. Ra12 compositions and methods for their use in enhancing the expression
20 and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent
25 and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; *see also, Skeiky et al., Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference). C-terminal fragments of the MTB32A coding sequence express at high levels and remain as a soluble polypeptides throughout the
30 purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous

immunogenic polypeptides with which it is fused. One preferred Ra12 fusion polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A.

Other preferred Ra12 polynucleotides generally comprise at least about
5 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide.

Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may
10 comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most
15 preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises
20 approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer).
25 The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein
30 known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is

derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion polypeptide. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as described in U.S. Patent No. 5,633,234. An immunogenic polypeptide of the invention, when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of CD4⁺ T-cells specific for the polypeptide.

Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See Merrifield, J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

In general, polypeptide compositions (including fusion polypeptides) of the invention are isolated. An "isolated" polypeptide is one that is removed from its original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure.

Polynucleotide Compositions

The present invention, in other aspects, provides polynucleotide compositions. The terms "DNA" and "polynucleotide" are used essentially interchangeably herein to refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the

present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or
5 may comprise a sequence that encodes a variant or derivative, preferably and immunogenic variant or derivative, of such a sequence.

Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49,
10 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467, complements of a polynucleotide sequence set forth in any one
15 of SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467, and degenerate
20 variants of a polynucleotide sequence set forth in any one of SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71, 73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420,
25 424, 428, 431, 434, 442, 447, 450 and 467. In certain preferred embodiments, the polynucleotide sequences set forth herein encode immunogenic polypeptides, as described above.

In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in
30 SEQ ID NOs:1-3, 6-8, 10-13, 15-27, 29, 30, 32, 34-49, 51, 52, 54, 55, 57-59, 61-69, 71,

73, 74, 77, 78, 80-82, 84, 86-96, 107-109, 111, 113, 125, 127, 128, 129, 131-133, 142, 144, 148-151, 153, 154, 157, 158, 160, 167, 168, 171, 179, 182, 184-186, 188-191, 193, 194, 198-207, 209, 210, 213, 214, 217, 220-224, 253-337, 345, 347, 349, 358, 362, 364, 365, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467, for example those
5 comprising at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide sequence of this invention using the methods described herein, (e.g., BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine
10 corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the
15 polypeptide encoded by the variant polynucleotide is not substantially diminished relative to a polypeptide encoded by a polynucleotide sequence specifically set forth herein). The term "variants" should also be understood to encompass homologous genes of xenogenic origin.

In additional embodiments, the present invention provides
20 polynucleotide fragments comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all
25 intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-60°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. One skilled in the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable highly stringent hybridization conditions include those described above, with the exception that the temperature of hybridization is increased, *e.g.*, to 60-65°C or 65-70°C.

In certain preferred embodiments, the polynucleotides described above, *e.g.*, polynucleotide variants, fragments and hybridizing sequences, encode polypeptides that are immunologically cross-reactive with a polypeptide sequence specifically set forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative polynucleotide segments with total lengths of about 10,000, about

5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

When comparing polynucleotide sequences, two sequences are said to be
5 “identical” if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A “comparison window” as used herein, refers to a segment of at least about 20 contiguous positions,
10 usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR,
15 Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990)
20 Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and*
25 *Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J.*
30 *Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988)

Proc. Natl. Acad. Sci. USA 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

5 One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent
10 sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of
15 the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for
20 nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

 Preferably, the "percentage of sequence identity" is determined by
25 comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The
30 percentage is calculated by determining the number of positions at which the identical

nucleic acid bases occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

5 It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present
10 invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard
15 techniques (such as hybridization, amplification and/or database sequence comparison).

 Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of immunogenic variants and/or derivatives of the polypeptides described herein. By this approach, specific modifications in a polypeptide sequence can be made through
20 mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the polynucleotide.

 Site-specific mutagenesis allows the production of mutants through the
25 use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise

change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25 nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be
5 obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

10 As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed
15 mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson, 1987). Typically,
20 vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

In another approach for the production of polypeptide variants of the
25 present invention, recursive sequence recombination, as described in U.S. Patent No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

In other embodiments of the present invention, the polynucleotide
30 sequences provided herein can be advantageously used as probes or primers for nucleic

acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 nucleotide long contiguous sequence that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence disclosed herein will find particular utility. Longer contiguous identical or
5 complementary sequences, *e.g.*, those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a sequence of interest will enable them to be of use in detecting the presence of
10 complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides
15 or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in various bacterial cells. The total size of fragment, as well as the size of the
20 complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger contiguous complementarity stretches may be used, according to the length
25 complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in length are generally preferred, though, in order to increase stability and selectivity of the
30 hybrid, and thereby improve the quality and degree of specific hybrid molecules

obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR™ technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, *e.g.*, one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one
5 may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to
10 destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

According to another embodiment of the present invention, polynucleotide compositions comprising antisense oligonucleotides are provided.
15 Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein synthesis, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis is well established. For example, the synthesis of polygalacturonase and the muscarine
20 type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, striatal GABA_A receptor and human EGF (Jaskulski *et al.*, Science. 1988 Jun
25 10;240(4858):1544-6; Vasanthakumar and Ahmed, Cancer Commun. 1989;1(4):225-32; Peris *et al.*, Brain Res Mol Brain Res. 1998 Jun 15;57(2):310-20; U. S. Patent 5,801,154; U.S. Patent 5,789,573; U. S. Patent 5,718,709 and U.S. Patent 5,610,288). Antisense constructs have also been described that inhibit and can be used to treat a variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S.
30 Patent 5,591,317 and U. S. Patent 5,783,683).

Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein, or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In each case, preferred compositions comprise a sequence region that is complementary, and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure, T_m , binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations can be performed, for example, using v.4 of the OLIGO primer analysis software and/or the BLASTN 2.0.5 algorithm software (Altschul *et al.*, Nucleic Acids Res. 1997, 25(17):3389-402).

The use of an antisense delivery method employing a short peptide vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, Nucleic Acids Res. 1997 Jul 15;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%).

Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, Proc Natl Acad Sci U S A. 1987 Dec;84(24):8788-92; Forster and Symons, Cell. 1987 Apr 24;49(2):211-20). For example, a large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, Cell. 1981 Dec;27(3 Pt 2):487-96; Michel and Westhof, J Mol Biol. 1990 Dec 5;216(3):585-610; Reinhold-Hurek and Shub, Nature. 1992 May 14;357(6374):173-6). This specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many technologies, such as antisense technology (where a nucleic acid molecule simply binds

to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of
5 target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action
10 (Woolf *et al.*, Proc Natl Acad Sci U S A. 1992 Aug 15;89(16):7305-9). Thus, the specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis δ virus, group I intron or RNaseP RNA (in association with an RNA
15 guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* Nucleic Acids Res. 1992 Sep 11;20(17):4559-65. Examples of hairpin motifs are described by Hampel *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz, Biochemistry 1989 Jun 13;28(12):4929-33; Hampel *et al.*, Nucleic Acids Res. 1990 Jan 25;18(2):299-304 and U. S. Patent 5,631,359. An example of the
20 hepatitis δ virus motif is described by Perrotta and Been, Biochemistry. 1992 Dec 1;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada *et al.*, Cell. 1983 Dec;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, Cell. 1990 May 18;61(4):685-96; Saville and Collins, Proc Natl Acad Sci U S A. 1991 Oct 1;88(19):8826-30; Collins and Olive,
25 Biochemistry. 1993 Mar 23;32(11):2795-9); and an example of the Group I intron is described in (U. S. Patent 4,987,071). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an

RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically
5 incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Ribozyme activity can be optimized by altering the length of the
10 ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO 92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can
15 be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be
20 administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles.
25 Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stint. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions
30 of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO

94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression
5 vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby.
10 Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells. Ribozymes expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA
15 vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, *Antisense Nucleic Acid Drug*
20 *Dev.* 1997 7(4) 431-37). PNA is able to be utilized in a number methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997
25 Jun;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, *Science* 1991 Dec 6;254(5037):1497-500; Hanvey *et al.*, *Science*. 1992 Nov 27;258(5087):1481-5; Hyrup and Nielsen, *Bioorg Med Chem*. 1996 Jan;4(1):5-23). This chemistry has three important
5 consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.

10 PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*, *Bioorg Med Chem*. 1995 Apr;3(4):437-45). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of
15 closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this
20 difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography, providing yields and purity of product similar to those observed during the synthesis of peptides.

25 Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or
30 for specific functional requirements. Once synthesized, the identity of PNAs and their

derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (for example, Norton *et al.*, *Bioorg Med Chem.* 1995 Apr;3(4):437-45; Petersen *et al.*, *J Pept Sci.* 1995 May-Jun;1(3):175-83; Orum *et al.*, *Biotechniques.* 1995 Sep;19(3):472-80; Footer *et al.*, *Biochemistry.* 1996 Aug 20;35(33):10673-9; Griffith *et al.*, *Nucleic Acids Res.* 1995 Aug 11;23(15):3003-8; Pardridge *et al.*, *Proc Natl Acad Sci U S A.* 1995 Jun 6;92(12):5592-6; Boffa *et al.*, *Proc Natl Acad Sci U S A.* 1995 Mar 14;92(6):1901-5; Gambacorti-Passerini *et al.*, *Blood.* 1996 Aug 15;88(4):1411-7; Armitage *et al.*, *Proc Natl Acad Sci U S A.* 1997 Nov 11;94(23):12320-5; Seeger *et al.*, *Biotechniques.* 1997 Sep;23(3):512-7). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (*Anal Chem.* 1993 Dec 15;65(24):3545-9) and Jensen *et al.* (*Biochemistry.* 1997 Apr 22;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, mutational analysis, enhancers of transcription, nucleic acid purification, isolation of transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, *in situ* hybridization, and the like.

Polynucleotide Identification, Characterization and Expression

Polynucleotides compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques (see generally, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by

screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least two fold greater in a tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as tumor cells.

Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCRTM) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by reference in its entirety. Briefly, in PCRTM, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse transcription and PCRTM amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Any of a number of other template dependent processes, many of which are variations of the PCRTM amplification technique, are readily known and available in the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Patent No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain

Reaction (RCR). Still other amplification methods are described in Great Britain Pat. Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence
5 based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA
10 ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara, 1989) are also well-known to those of skill in the art.

An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (*e.g.*, a tumor cDNA library)
15 using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

20 For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ³²P) using well known techniques. A bacterial or bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor
25 Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The
30 complete sequence may then be determined using standard techniques, which may

involve generating a series of deletion clones. The resulting overlapping sequences can then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, amplification techniques, such as those described above,
5 can be useful for obtaining a full length coding sequence from a partial cDNA sequence. One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region.
10 Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate
15 extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et
20 al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as
25 that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

In other embodiments of the invention, polynucleotide sequences or
30 fragments thereof which encode polypeptides of the invention, or fusion proteins or

functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may
5 be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression
10 or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide
15 encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction
20 sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of
25 polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical
5 methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science* 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

10 A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) *Proteins, Structures and Molecular Principles*, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation
15 procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate
20 expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA
25 techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook, J. et al. (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, N.Y.

A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors;
5 insect cell systems infected with virus expression vectors (*e.g.*, baculovirus); plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" present in an
10 expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used.
15 For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains multiple
20 copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors
25 which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of β -galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S.
30

M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose
5 beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing
10 constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For
15 example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991)
20 *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

25 An insect system may also be used to express a polypeptide of interest. For example, in one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control
30 of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence

will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia* larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci.* 91 :3224-3227).

5 In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used
10 to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

 Specific initiation signals may also be used to achieve more efficient
15 translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion
20 thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are
25 appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

 In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to,
30 acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation.

Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate

luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. et al. (1995) *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that
5 the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter.
10 Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells that contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-
15 RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies
20 specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed.
25 These and other assays are described, among other places, in Hampton, R. et al. (1990; *Serological Methods, a Laboratory Manual*, APS Press, St Paul, Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med.* 158:1211-1216).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means
30 for producing labeled hybridization or PCR probes for detecting sequences related to

polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase

cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; *DNA Cell Biol.* 12:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

Antibody Compositions, Fragments Thereof and Other Binding Agents

According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunologically bind," and/or is "immunologically reactive" to a polypeptide of the invention if it reacts at a detectable level (within, for example, an ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and

on geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" (K_{on}) and the "off rate constant" (K_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of K_{off}/K_{on} enables cancellation of all parameters not related to affinity, and is thus equal to the dissociation constant K_d . See, generally, Davies et al. (1990) Annual Rev. Biochem. 59:439-473.

An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

Binding agents may be further capable of differentiating between patients with and without a cancer, such as lung cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein

for the presence of polypeptides that bind to the binding agent. Preferably, a statistically significant number of samples with and without the disease will be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve
5 sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of
10 a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of
15 recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier
20 protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a
25 suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the
30 desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may

be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells
5 and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture
10 supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable
15 vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

20 A number of therapeutically useful molecules are known in the art which comprise antigen-binding sites that are capable of exhibiting immunological binding properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The
25 enzyme pepsin is able to cleave IgG molecules to provide several fragments, including the "F(ab)₂" fragment which comprises both antigen-binding sites. An "Fv" fragment can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a
30 non-covalent V_H::V_L heterodimer including an antigen-binding site which retains much

of the antigen recognition and binding capabilities of the native antibody molecule. Inbar et al. (1972) Proc. Nat. Acad. Sci. USA 69:2659-2662; Hochman et al. (1976) Biochem 15:2706-2710; and Ehrlich et al. (1980) Biochem 19:4091-4096.

A single chain Fv ("sFv") polypeptide is a covalently linked $V_H::V_L$ heterodimer which is expressed from a gene fusion including V_H - and V_L -encoding genes linked by a peptide-encoding linker. Huston et al. (1988) Proc. Nat. Acad. Sci. USA 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated—but chemically separated—light and heavy polypeptide chains from an antibody V region into an sFv molecule which will fold into a three dimensional structure substantially similar to the structure of an antigen-binding site. See, e.g., U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.; and U.S. Pat. No. 4,946,778, to Ladner et al.

Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRs and define the spatial relationship of the CDRs relative to each other. As used herein, the term "CDR set" refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-terminus of a heavy or light chain, these regions are denoted as "CDR1," "CDR2," and "CDR3" respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (e.g., a CDR1, CDR2 or CDR3) is referred to herein as a "molecular recognition unit." Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

As used herein, the term "FR set" refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues

directly adjacent to the CDRs. Within FRs, certain amino residues and certain structural features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain "canonical" structures--regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

10 A number of "humanized" antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) *Nature* 349:293-299; Lobuglio et al. (1989) *Proc. Nat. Acad. Sci. USA* 86:4220-4224; Shaw et al. (1987) *J Immunol.* 138:4534-15 4538; and Brown et al. (1987) *Cancer Res.* 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant domain (Riechmann et al. (1988) *Nature* 332:323-327; Verhoeven et al. (1988) *Science* 239:1534-1536; and Jones et al. (1986) *Nature* 321:522-525), and rodent CDRs supported by recombinantly veneered rodent FRs (European Patent Publication No. 20 519,596, published Dec. 23, 1992). These "humanized" molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

As used herein, the terms "veneered FRs" and "recombinantly veneered FRs" refer to the selective replacement of FR residues from, *e.g.*, a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the ligand binding characteristics of an antigen-binding site are determined primarily by 30 the structure and relative disposition of the heavy and light chain CDR sets within the

antigen-binding surface. Davies et al. (1990) Ann. Rev. Biochem. 59:439-473. Thus, antigen binding specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other, and their interaction with the rest of the V region domains are carefully maintained. By using veneering techniques, exterior
5 (e.g., solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

The process of veneering makes use of the available sequence data for
10 human antibody variable domains compiled by Kabat et al., in Sequences of Proteins of Immunological Interest, 4th ed., (U.S. Dept. of Health and Human Services, U.S. Government Printing Office, 1987), updates to the Kabat database, and other accessible U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V region amino acids can be deduced from the known three-dimensional structure for
15 human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody molecule of interest are compared with corresponding FR sequences of human variable domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The
20 residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the art. Residue switching is only carried out with moieties which are at least partially exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region
25 domains, such as proline, glycine and charged amino acids.

In this manner, the resultant "veneered" murine antigen-binding sites are thus designed to retain the murine CDR residues, the residues substantially adjacent to the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (e.g., electrostatic and hydrophobic)
30 contacts between heavy and light chain domains, and the residues from conserved

structural regions of the FRs which are believed to influence the "canonical" tertiary structures of the CDR loops. These design criteria are then used to prepare recombinant nucleotide sequences which combine the CDRs of both the heavy and light chain of a murine antigen-binding site into human-appearing FRs that can be used to transfect
5 mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

In another embodiment of the invention, monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and
10 ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a
15 suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-
20 containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker
25 group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional
30 or polyfunctional reagents, both homo- and hetero-functional (such as those described in

the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

5 Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction
10 of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

15 It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be
20 coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

 A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides
25 such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative
30 radiohalogenated small molecules and their synthesis. A radionuclide chelate may be

formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

5 T Cell Compositions

The present invention, in another aspect, provides T cells specific for a tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone
10 marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

15 T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor polypeptide or polynucleotide of the invention is present within a delivery vehicle, such
20 as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a polypeptide of the present invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For
25 example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For

example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Tumor polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

25

T Cell Receptor Compositions

The T cell receptor (TCR) consists of 2 different, highly variable polypeptide chains, termed the T-cell receptor α and β chains, that are linked by a disulfide bond (Janeway, Travers, Walport. *Immunobiology*. Fourth Ed., 148-159.

Elsevier Science Ltd/Garland Publishing. 1999). The α/β heterodimer complexes with the invariant CD3 chains at the cell membrane. This complex recognizes specific antigenic peptides bound to MHC molecules. The enormous diversity of TCR specificities is generated much like immunoglobulin diversity, through somatic gene rearrangement. The β chain genes contain over 50 variable (V), 2 diversity (D), over 10 joining (J) segments, and 2 constant region segments (C). The α chain genes contain over 70 V segments, and over 60 J segments but no D segments, as well as one C segment. During T cell development in the thymus, the D to J gene rearrangement of the β chain occurs, followed by the V gene segment rearrangement to the DJ. This functional VDJ β exon is transcribed and spliced to join to a C β . For the α chain, a V α gene segment rearranges to a J α gene segment to create the functional exon that is then transcribed and spliced to the C α . Diversity is further increased during the recombination process by the random addition of P and N-nucleotides between the V, D, and J segments of the β chain and between the V and J segments in the α chain (Janeway, Travers, Walport. *Immunobiology*. Fourth Ed., 98 and 150. Elsevier Science Ltd/Garland Publishing. 1999).

The present invention, in another aspect, provides TCRs specific for a polypeptide disclosed herein, or for a variant or derivative thereof. In accordance with the present invention, polynucleotide and amino acid sequences are provided for the V-J or V-D-J junctional regions or parts thereof for the alpha and beta chains of the T-cell receptor which recognize tumor polypeptides described herein. In general, this aspect of the invention relates to T-cell receptors which recognize or bind tumor polypeptides presented in the context of MHC. In a preferred embodiment the tumor antigens recognized by the T-cell receptors comprise a polypeptide of the present invention. For example, cDNA encoding a TCR specific for a _tumor peptide can be isolated from T cells specific for a tumor polypeptide using standard molecular biological and recombinant DNA techniques.

This invention further includes the T-cell receptors or analogs thereof having substantially the same function or activity as the T-cell receptors of this invention which recognize or bind tumor polypeptides. Such receptors include, but are

not limited to, a fragment of the receptor, or a substitution, addition or deletion mutant of a T-cell receptor provided herein. This invention also encompasses polypeptides or peptides that are substantially homologous to the T-cell receptors provided herein or that retain substantially the same activity. The term "analog" includes any protein or
5 polypeptide having an amino acid residue sequence substantially identical to the T-cell receptors provided herein in which one or more residues, preferably no more than 5 residues, more preferably no more than 25 residues have been conservatively substituted with a functionally similar residue and which displays the functional aspects of the T-cell receptor as described herein.

10 The present invention further provides for suitable mammalian host cells, for example, non-specific T cells, that are transfected with a polynucleotide encoding TCRs specific for a polypeptide described herein, thereby rendering the host cell specific for the polypeptide. The α and β chains of the TCR may be contained on separate expression vectors or alternatively, on a single expression vector that also
15 contains an internal ribosome entry site (IRES) for cap-independent translation of the gene downstream of the IRES. Said host cells expressing TCRs specific for the polypeptide may be used, for example, for adoptive immunotherapy of lung cancer as discussed further below.

In further aspects of the present invention, cloned TCRs specific for a
20 polypeptide recited herein may be used in a kit for the diagnosis of lung cancer. For example, the nucleic acid sequence or portions thereof, of tumor-specific TCRs can be used as probes or primers for the detection of expression of the rearranged genes encoding the specific TCR in a biological sample. Therefore, the present invention further provides for an assay for detecting messenger RNA or DNA encoding the TCR
25 specific for a polypeptide.

Pharmaceutical Compositions

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions

disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other
5 proteins or polypeptides or various pharmaceutically-active agents. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from
10 host cells or other biological sources, or alternatively may be chemically synthesized as described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

Therefore, in another aspect of the present invention, pharmaceutical compositions are provided comprising one or more of the polynucleotide, polypeptide,
15 antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide and/or polypeptide compositions of the invention for use in prophylactic and therapeutic vaccine applications. Vaccine preparation is generally described in, for example, M.F.
20 Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination with one or more immunostimulants.

It will be apparent that any of the pharmaceutical compositions described
25 herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.*, salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.*, sodium, potassium, lithium, ammonium, calcium and magnesium salts).

In another embodiment, illustrative immunogenic compositions, *e.g.*, vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the polynucleotide may be administered within any of a variety of delivery systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary regulatory DNA regulatory sequences for expression in a patient (such as a suitable promoter and terminating signal). Alternatively, bacterial delivery systems may involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

Therefore, in certain embodiments, polynucleotides encoding immunogenic polypeptides described herein are introduced into suitable mammalian host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to a subject. A number of illustrative retroviral systems have been described (*e.g.*, U.S. Pat. No. 5,219,740; Miller and Rosman (1989) *BioTechniques* 7:980-990; Miller, A. D. (1990) *Human Gene Therapy* 1:5-14; Scarpa et al. (1991) *Virology* 180:849-852; Burns et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:8033-8037; and Boris-Lawrie and Temin (1993) *Cur. Opin. Genet. Develop.* 3:102-109.

In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) *J. Virol.* 57:267-274; Bett et al. (1993) *J. Virol.* 67:5911-5921; Mittereder et al. (1994) *Human Gene Therapy* 5:717-729; Seth et al. (1994) *J. Virol.* 68:933-940; Barr et al. (1994) *Gene Therapy* 1:51-58; Berkner, K. L.

(1988) *BioTechniques* 6:616-629; and Rich et al. (1993) *Human Gene Therapy* 4:461-476).

Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using techniques well known in the art. See, e.g., U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) *Molec. Cell. Biol.* 8:3988-3996; Vincent et al. (1990) *Vaccines 90* (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) *Current Opinion in Biotechnology* 3:533-539; Muzyczka, N. (1992) *Current Topics in Microbiol. and Immunol.* 158:97-129; Kotin, R. M. (1994) *Human Gene Therapy* 5:793-801; Shelling and Smith (1994) *Gene Therapy* 1:165-169; and Zhou et al. (1994) *J. Exp. Med.* 179:1867-1875.

Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the polypeptide of interest into the viral genome. The resulting TK.sup.(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide or polynucleotides of interest, driven by a T7

promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, *e.g.*, Elroy-Stein and Moss, *Proc. Natl. Acad. Sci. USA* (1990) 87:6743-6747; Fuerst et al. *Proc. Natl. Acad. Sci. USA* (1986) 83:8122-8126.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant Avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, *e.g.*, WO 91/12882; WO 89/03429; and WO 92/03545.

Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in U.S. Patent Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Patent Nos. 5,505,947 and 5,643,576.

Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. *J. Biol. Chem.* (1993) 268:6866-6869 and Wagner et al. *Proc. Natl. Acad. Sci. USA* (1992) 89:6099-6103, can also be used for gene delivery under the invention.

Additional illustrative information on these and other known viral-based delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242;

WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993.

5 In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in the specific location and orientation via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the polynucleotide may be stably maintained in the cell as a separate, episomal segment of
10 DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. The manner in which the expression construct is delivered to a cell and where in the cell the polynucleotide remains is dependent on the type of expression construct employed.

15 In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

20 In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described. In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK) and Powderject Vaccines Inc. (Madison, WI), some examples of which are described in
25 U.S. Patent Nos. 5,846,796; 6,010,478; 5,865,796; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to high speed within a helium gas jet generated by a hand held device, propelling the particles into a target tissue of interest.

In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include those provided by Bioject, Inc. (Portland, OR), some examples of which are described in U.S. Patent Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639
5 and 5,993,412.

According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances
10 or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins.
15 Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated
20 sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Within certain embodiments of the invention, the adjuvant composition
25 is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as
30 provided herein, a patient will support an immune response that includes Th1- and Th2-

type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman,
5 *Ann. Rev. Immunol.* 7:145-173, 1989.

Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL® adjuvants are available from Corixa Corporation (Seattle, WA; *see*, for example, US
10 Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by
15 Sato et al., *Science* 273:352, 1996. Another preferred adjuvant comprises a saponin, such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, MA); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins. Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example
20 combinations of at least two of the following group comprising QS21, QS7, Quil A, β -escin, or digitonin.

Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and polylactide-co-glycolide particles, poly-N-acetyl glucosamine-based polymer matrix,
25 particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated together with a polyoxyethylene ether or ester, in either a non-particulate solution or
30 suspension, or in a particulate structure such as a paucilamellar liposome or ISCOM. The

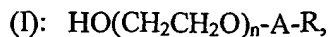
saponins may also be formulated with excipients such as Carbopol^R to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

In one preferred embodiment, the adjuvant system includes the
5 combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL[®] adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-
10 MPL[®] adjuvant and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Another enhanced adjuvant system involves the combination of a CpG-containing oligonucleotide and a saponin derivative particularly the combination of CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally
15 comprises an oil in water emulsion and tocopherol.

Additional illustrative adjuvants for use in the pharmaceutical compositions of the invention include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart,
20 Belgium), Detox (Enhanzyn[®]) (Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties, and polyoxyethylene ether adjuvants such as those described in WO 99/52549A1.

25 Other preferred adjuvants include adjuvant molecules of the general formula



wherein, n is 1-50, A is a bond or $-\text{C}(\text{O})-$, R is C_{1-50} alkyl or Phenyl C_{1-50} alkyl.

One embodiment of the present invention consists of a vaccine
30 formulation comprising a polyoxyethylene ether of general formula (I), wherein n is

between 1 and 50, preferably 4-24, most preferably 9; the *R* component is C₁₋₅₀, preferably C_{4-C20} alkyl and most preferably C₁₂ alkyl, and *A* is a bond. The concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene
5 ethers are selected from the following group: polyoxyethylene-9-lauryl ether, polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether. Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck index (12th edition: entry 7717). These adjuvant molecules are described in WO
10 99/52549.

The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant combination is preferably with CpG as described in the pending UK patent application GB 9820956.2.

15 According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or
20 maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

25 Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In
30 general, dendritic cells may be identified based on their typical shape (*stellate in situ*,

with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see Zitvogel et al., Nature Med. 4:594-600, 1998*).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide of the invention (or portion or other variant thereof) such that the encoded polypeptide, or an

immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will typically vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

Carriers for use within such pharmaceutical compositions are biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release. In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the level of ordinary skill in the art using known techniques. Illustrative carriers useful in this regard include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*,

a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends
5 upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

In another illustrative embodiment, biodegradable microspheres (*e.g.*, polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S.
10 Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763; 5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems, such as described in WO/99 40934, and references cited therein, will also be useful for many applications. Another illustrative carrier/delivery system employs a carrier comprising particulate-protein complexes, such as those described in U.S. Patent No.
15 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

The pharmaceutical compositions of the invention will often further comprise one or more buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins,
20 polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate.

25 The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are typically sealed in such a way to preserve the sterility and stability of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a pharmaceutical composition

may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including
5 e.g., oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art, some of which are briefly discussed below for general purposes of illustration.

In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions
10 may be formulated with an inert diluent or with an assimilable edible carrier, or they may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs,
15 suspensions, syrups, wafers, and the like (see, for example, Mathiowitz *et al.*, Nature 1997 Mar 27;386(6623):410-4; Hwang *et al.*, Crit Rev Ther Drug Carrier Syst 1998;15(3):243-84; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia,
20 cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to
25 materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds
30 may be incorporated into sustained-release preparation and formulations.

Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared is such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

For oral administration the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363. In certain embodiments, solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain a preservative to prevent the growth of microorganisms.

Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U. S. Patent 5,466,468). In all cases the form must be sterile and must be fluid to the extent that
5 easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable
10 oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be
15 preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

In one embodiment, for parenteral administration in an aqueous solution,
20 the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one
25 dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of

course preferably meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

In another embodiment of the invention, the compositions disclosed herein may be formulated in a neutral or salt form. Illustrative
5 pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium,
10 calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

The carriers can further comprise any and all solvents, dispersion media,
15 vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary
20 active ingredients can also be incorporated into the compositions. The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles.
25 Methods for delivering genes, nucleic acids, and peptide compositions directly to the lungs *via* nasal aerosol sprays has been described, *e.g.*, in U. S. Patent 5,756,353 and U. S. Patent 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, *J Controlled Release* 1998 Mar 2;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871) are also well-known in

the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of a polytetrafluoroethylene support matrix is described in U. S. Patent 5,780,045.

In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

The formation and use of liposome and liposome-like preparations as potential drug carriers is generally known to those of skill in the art (see for example, Lasic, Trends Biotechnol 1998 Jul;16(7):307-21; Takakura, Nippon Rinsho 1998 Mar;56(3):691-5; Chandran *et al.*, Indian J Exp Biol. 1997 Aug;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, J Biol Chem. 1990 Sep 25;265(27):16337-42; Muller *et al.*, DNA Cell Biol. 1990 Apr;9(3):221-9). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, various drugs, radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, the use of liposomes does not appear to be associated with autoimmune responses or unacceptable toxicity after systemic delivery.

In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)).

Alternatively, in other embodiments, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero *et al.*, Drug Dev Ind Pharm. 5 1998 Dec;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) may be designed using polymers able to be degraded *in vivo*. Such particles can be made as described, for example, by Couvreur *et al.*, Crit Rev Ther Drug Carrier Syst. 1988;5(1):1-20; zur Muhlen *et al.*, Eur J Pharm Biopharm. 1998 Mar;45(2):149-55; Zambaux *et al.* J 10 Controlled Release. 1998 Jan 2;50(1-3):31-40; and U. S. Patent 5,145,684.

Cancer Therapeutic Methods

Immunologic approaches to cancer therapy are based on the recognition that cancer cells can often evade the body's defenses against aberrant or foreign cells and molecules, and that these defenses might be therapeutically stimulated to regain the 15 lost ground, *e.g.* pgs. 623-648 in Klein, Immunology (Wiley-Interscience, New York, 1982). Numerous recent observations that various immune effectors can directly or indirectly inhibit growth of tumors has led to renewed interest in this approach to cancer therapy, *e.g.* Jager, *et al.*, Oncology 2001;60(1):1-7; Renner, *et al.*, Ann Hematol 2000 Dec;79(12):651-9.

20 Four-basic cell types whose function has been associated with antitumor cell immunity and the elimination of tumor cells from the body are: i) B-lymphocytes which secrete immunoglobulins into the blood plasma for identifying and labeling the nonself invader cells; ii) monocytes which secrete the complement proteins that are responsible for lysing and processing the immunoglobulin-coated target invader cells; 25 iii) natural killer lymphocytes having two mechanisms for the destruction of tumor cells, antibody-dependent cellular cytotoxicity and natural killing; and iv) T-lymphocytes possessing antigen-specific receptors and having the capacity to recognize a tumor cell carrying complementary marker molecules (Schreiber, H., 1989, in Fundamental Immunology (ed). W. E. Paul, pp. 923-955).

Cancer immunotherapy generally focuses on inducing humoral immune responses, cellular immune responses, or both. Moreover, it is well established that induction of CD4⁺ T helper cells is necessary in order to secondarily induce either antibodies or cytotoxic CD8⁺ T cells. Polypeptide antigens that are selective or ideally
5 specific for cancer cells, particularly lung cancer cells, offer a powerful approach for inducing immune responses against lung cancer, and are an important aspect of the present invention.

Therefore, in further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for
10 the immunotherapy of lung cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical
15 compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal,
20 anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided
25 herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host
30 immune system. Examples of effector cells include T cells as discussed above, T

lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody
5 receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

10 Monoclonal antibodies may be labeled with any of a variety of labels for desired selective usages in detection, diagnostic assays or therapeutic applications (as described in U.S. Patent Nos. 6,090,365; 6,015,542; 5,843,398; 5,595,721; and 4,708,930, hereby incorporated by reference in their entirety as if each was incorporated individually). In each case, the binding of the labelled monoclonal antibody to the
15 determinant site of the antigen will signal detection or delivery of a particular therapeutic agent to the antigenic determinant on the non-normal cell. A further object of this invention is to provide the specific monoclonal antibody suitably labelled for achieving such desired selective usages thereof.

Effector cells may generally be obtained in sufficient quantities for
20 adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above,
25 immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known
30 in the art. For example, antigen-presenting cells can be transfected with a

polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive
5 long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced
10 into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical
15 compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for
20 individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor
25 cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose

ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

Cancer Detection and Diagnostic Compositions, Methods and Kits

In general, a cancer may be detected in a patient based on the presence of one or more lung tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as lung cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample.

Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a tumor sequence should be present at a level that is at least two-fold, preferably three-fold, and more preferably five-fold or higher in tumor tissue than in normal tissue of the same type from which the tumor arose. Expression levels of a particular tumor sequence in tissue types different from that in which the tumor arose are irrelevant in certain diagnostic embodiments since the presence of tumor cells can be confirmed by observation of predetermined differential expression levels, *e.g.*, 2-fold, 5-fold, etc, in tumor tissue to expression levels in normal tissue of the same type.

Other differential expression patterns can be utilized advantageously for diagnostic purposes. For example, in one aspect of the invention, overexpression of a tumor sequence in tumor tissue and normal tissue of the same type, but not in other normal tissue types, e.g. PBMCs, can be exploited diagnostically. In this case, the presence of metastatic tumor cells, for example in a sample taken from the circulation or some other tissue site different from that in which the tumor arose, can be identified and/or confirmed by detecting expression of the tumor sequence in the sample, for example using RT-PCR analysis. In many instances, it will be desired to enrich for tumor cells in the sample of interest, e.g., PBMCs, using cell capture or other like techniques.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length lung tumor

proteins and polypeptide portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support
5 may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support
10 using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent).
15 Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or
20 polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with
25 both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at
30 A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. 5 Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

10 More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to 15 bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with lung cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of 20 that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

25 Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody- 30 polypeptide complex for an amount of time sufficient to detect the bound polypeptide.

An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For
5 radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a
10 specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as lung cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In
15 one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a
20 Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off
25 value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In

general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use tumor polypeptides to detect antibodies that bind to such polypeptides in a biological

sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within
5 certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For
10 example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is
15 preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on
20 the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is
25 then separated and detected using techniques well known in the art, such as gel electrophoresis.

Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a tumor protein of the invention that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another aspect of the present invention, cell capture technologies may be used in conjunction, with, for example, real-time PCR to provide a more sensitive tool for detection of metastatic cells expressing lung tumor antigens. Detection of lung cancer cells in biological samples, e.g., bone marrow samples, peripheral blood, and

small needle aspiration samples is desirable for diagnosis and prognosis in lung cancer patients.

Immunomagnetic beads coated with specific monoclonal antibodies to surface cell markers, or tetrameric antibody complexes, may be used to first enrich or positively select cancer cells in a sample. Various commercially available kits may be used, including Dynabeads® Epithelial Enrich (DynaL Biotech, Oslo, Norway), StemSep™ (StemCell Technologies, Inc., Vancouver, BC), and RosetteSep (StemCell Technologies). A skilled artisan will recognize that other methodologies and kits may also be used to enrich or positively select desired cell populations. Dynabeads® Epithelial Enrich contains magnetic beads coated with mAbs specific for two glycoprotein membrane antigens expressed on normal and neoplastic epithelial tissues. The coated beads may be added to a sample and the sample then applied to a magnet, thereby capturing the cells bound to the beads. The unwanted cells are washed away and the magnetically isolated cells eluted from the beads and used in further analyses.

RosetteSep can be used to enrich cells directly from a blood sample and consists of a cocktail of tetrameric antibodies that targets a variety of unwanted cells and crosslinks them to glycophorin A on red blood cells (RBC) present in the sample, forming rosettes. When centrifuged over Ficoll, targeted cells pellet along with the free RBC. The combination of antibodies in the depletion cocktail determines which cells will be removed and consequently which cells will be recovered. Antibodies that are available include, but are not limited to: CD2, CD3, CD4, CD5, CD8, CD10, CD11b, CD14, CD15, CD16, CD19, CD20, CD24, CD25, CD29, CD33, CD34, CD36, CD38, CD41, CD45, CD45RA, CD45RO, CD56, CD66B, CD66e, HLA-DR, IgE, and TCR $\alpha\beta$.

Additionally, it is contemplated in the present invention that mAbs specific for lung tumor antigens can be generated and used in a similar manner. For example, mAbs that bind to tumor-specific cell surface antigens may be conjugated to magnetic beads, or formulated in a tetrameric antibody complex, and used to enrich or positively select metastatic lung tumor cells from a sample. Once a sample is enriched or positively selected, cells may be lysed and RNA isolated. RNA may then be subjected to RT-PCR analysis using lung tumor-specific primers in a real-time PCR

assay as described herein. One skilled in the art will recognize that enriched or selected populations of cells may be analyzed by other methods (e.g. *in situ* hybridization or flow cytometry).

In another embodiment, the compositions described herein may be used
5 as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the
10 level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound
15 binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific
20 for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

25 The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein.
30 Such antibodies or fragments may be provided attached to a support material, as

described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

5 Alternatively, a kit may be designed to detect the level of mRNA encoding a tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be
10 present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

 The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF cDNA SEQUENCES ENCODING LUNG TUMOR POLYPEPTIDES

This example illustrates the isolation of cDNA molecules encoding lung tumor-specific polypeptides from lung tumor cDNA libraries.

A. ISOLATION OF cDNA SEQUENCES FROM A LUNG SQUAMOUS CELL CARCINOMA LIBRARY

A human lung squamous cell carcinoma cDNA expression library was constructed from poly A⁺ RNA from a pool of two patient tissues using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD) following the manufacturer's protocol. Specifically, lung carcinoma tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using an oligo dT cellulose column as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with BstXI/EcoRI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with cDNA size fractionation columns (BRL Life Technologies), the cDNA was ligated into the BstXI/NotI site of pcDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human lung cDNA expression library was prepared from a pool of four tissue specimens. The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The lung squamous cell carcinoma library contained 2.7×10^6 independent colonies, with 100% of clones having an insert and the average insert size being 2100 base pairs. The normal

lung cDNA library contained 1.4×10^6 independent colonies, with 90% of clones having inserts and the average insert size being 1800 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA

5 cDNA library subtraction was performed using the above lung squamous cell carcinoma and normal lung cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a lung squamous cell carcinoma-specific subtracted cDNA library was generated as follows. Normal tissue cDNA library (80 μ g) was digested with BamHI and XhoI, followed by a filling-in
10 reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 133 μ l of H₂O, heat-denatured and mixed with 133 μ l (133 μ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (67 μ l) was added
15 and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 μ l H₂O to form the driver DNA.

To form the tracer DNA, 10 μ g lung squamous cell carcinoma cDNA library was digested with NotI and SpeI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech, Palo Alto, CA). Typically, 5 μ g of
20 cDNA was recovered after the sizing column. Following ethanol precipitation, the tracer DNA was dissolved in 5 μ l H₂O. Tracer DNA was mixed with 15 μ l driver DNA and 20 μ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and
25 incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 μ l H₂O, mixed with 8 μ l driver DNA and 20 μ l of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After
30 removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

NotI/SpeI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a lung squamous cell carcinoma specific subtracted cDNA library (herein after referred to as "lung subtraction I").

5 A second lung squamous cell carcinoma specific subtracted cDNA library (referred to as "lung subtraction II") was generated in a similar way to the lung subtraction library I, except that eight frequently recovered genes from lung subtraction I were included in the driver DNA, and 24,000 independent clones were recovered.

To analyze the subtracted cDNA libraries, plasmid DNA was prepared
10 from 320 independent clones, randomly picked from the subtracted lung squamous cell carcinoma specific libraries. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A and/or Model 377 (Foster City, CA). The cDNA sequences for sixty isolated clones are provided in SEQ ID NO: 1-60. These sequences were
15 compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). No significant homologies were found to the sequences provided in SEQ ID NO: 2, 3, 19, 38 and 46. The sequences of SEQ ID NO: 1, 6-8, 10-13, 15, 17, 18, 20-27, 29, 30, 32, 34-37, 39-45, 47-49, 51, 52, 54, 55 and 57-59 were found to show some homology to previously identified expressed sequence tags (ESTs).
20 The sequences of SEQ ID NO: 9, 28, 31 and 33 were found to show some homology to previously identified non-human gene sequences and the sequences of SEQ ID NO: 4, 5, 14, 50, 53, 56 and 60 were found to show some homology to gene sequences previously identified in humans.

The subtraction procedure described above was repeated using the above
25 lung squamous cell carcinoma cDNA library as the tracer DNA, and the above normal lung tissue cDNA library and a cDNA library from normal liver and heart (constructed from a pool of one sample of each tissue as described above), plus twenty other cDNA clones that were frequently recovered in lung subtractions I and II, as the driver DNA (lung subtraction III). The normal liver and heart cDNA library contained 1.76×10^6
30 independent colonies, with 100% of clones having inserts and the average insert size

being 1600 base pairs. Ten additional clones were isolated (SEQ ID NO: 61-70). Comparison of these cDNA sequences with those in the gene bank as described above, revealed no significant homologies to the sequences provided in SEQ ID NO: 62 and 67. The sequences of SEQ ID NO: 61, 63-66, 68 and 69 were found to show some
5 homology to previously isolated ESTs and the sequence provided in SEQ ID NO: 70 was found to show some homology to a previously identified rat gene.

In further studies, the subtraction procedure described above was repeated using the above lung squamous cell carcinoma cDNA library as the tracer DNA, and a cDNA library from a pool of normal lung, kidney, colon, pancreas, brain,
10 resting PBMC, heart, skin and esophagus as the driver DNA, with esophagus cDNAs making up one third of the driver material. Since esophagus is enriched in normal epithelial cells, including differentiated squamous cells, this procedure is likely to enrich genes that are tumor specific rather than tissues specific. The cDNA sequences of 48 clones determined in this subtraction are provided in SEQ ID NO: 177-224. The
15 sequences of SEQ ID NO: 177, 178, 180, 181, 183, 187, 192, 195-197, 208, 211, 212, 215, 216, 218 and 219 showed some homology to previously identified genes. The sequences of SEQ ID NO: 179, 182, 184-186, 188-191, 193, 194, 198-207, 209 210, 213, 214, 217, 220 and 224 showed some homology to previously determined ESTs. The sequence of SEQ ID NO: 221-223 showed no homology to any previously
20 determined sequence.

B. ISOLATION OF cDNA SEQUENCES FROM A LUNG ADENOCARCINOMA LIBRARY

A human lung adenocarcinoma cDNA expression library was constructed as described above. The library contained 3.2×10^6 independent colonies,
25 with 100% of clones having an insert and the average insert size being 1500 base pairs. Library subtraction was performed as described above using the normal lung and normal liver and heart cDNA expression libraries described above as the driver DNA. Twenty-six hundred independent clones were recovered.

Initial cDNA sequence analysis from 100 independent clones revealed many ribosomal protein genes. The cDNA sequences for fifteen clones isolated in this subtraction are provided in SEQ ID NO: 71-86. Comparison of these sequences with those in the gene bank as described above revealed no significant homologies to the
5 sequence provided in SEQ ID NO: 84. The sequences of SEQ ID NO: 71, 73, 74, 77, 78 and 80-82 were found to show some homology to previously isolated ESTs, and the sequences of SEQ ID NO: 72, 75, 76, 79, 83 and 85 were found to show some homology to previously identified human genes.

In further studies, a cDNA library (referred to as mets3616A) was
10 constructed from a metastatic lung adenocarcinoma. The determined cDNA sequences of 25 clones sequenced at random from this library are provided in SEQ ID NO: 255-279. The mets3616A cDNA library was subtracted against a cDNA library prepared from a pool of normal lung, liver, pancreas, skin, kidney, brain and resting PBMC. To increase the specificity of the subtraction, the driver was spiked with genes that were
15 determined to be most abundant in the mets3616A cDNA library, such as EF1-alpha, integrin-beta and anticoagulant protein PP4, as well as with cDNAs that were previously found to be differentially expressed in subtracted lung adenocarcinoma cDNA libraries. The determined cDNA sequences of 51 clones isolated from the subtracted library (referred to as mets3616A-S1) are provided in SEQ ID NO: 280-330.

20 Comparison of the sequences of SEQ ID NO: 255-330 with those in the public databases revealed no significant homologies to the sequences of SEQ ID NO: 255-258, 260, 262-264, 270, 272, 275, 276, 279, 281, 287, 291, 296, 300 and 310. The sequences of SEQ ID NO: 259, 261, 265-269, 271, 273, 274, 277, 278, 282-285, 288-290, 292, 294, 297-299, 301, 303-309, 313, 314, 316, 320-324 and 326-330 showed
25 some homology to previously identified gene sequences, while the sequences of SEQ ID NO: 280, 286, 293, 302, 310, 312, 315, 317-319 and 325 showed some homology to previously isolated expressed sequence tags (ESTs).

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF LUNG TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for seven representative lung tumor polypeptides described in Example 1 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. 1 µl of 1:30 dilution of cDNA was employed to enable the linear range amplification of the β-actin template and was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in five different types of tumor tissue (lung squamous cell carcinoma from 3 patients, lung adenocarcinoma, colon tumor from 2 patients, breast tumor and prostate tumor), and thirteen different normal tissues (lung from 4 donors, prostate, brain, kidney, liver, ovary, skeletal muscle, skin, small intestine, stomach, myocardium, retina and testes). Using a 10-fold amount of cDNA, the antigen LST-S1-90 (SEQ ID NO: 3) was found to be expressed at high levels in lung squamous cell carcinoma and in breast tumor, and at low to undetectable levels in the other tissues examined.

The antigen LST-S2-68 (SEQ ID NO: 15) appears to be specific to lung and breast tumor, however, expression was also detected in normal kidney. Antigens LST-S1-169 (SEQ ID NO: 6) and LST-S1-133 (SEQ ID NO: 5) appear to be very abundant in lung tissues (both normal and tumor), with the expression of these two genes being decreased in most of the normal tissues tested. Both LST-S1-169 and LST-

S1-133 were also expressed in breast and colon tumors. Antigens LST-S1-6 (SEQ ID NO: 7) and LST-S2-I2-5F (SEQ ID NO: 47) did not show tumor or tissue specific expression, with the expression of LST-S1-28 being rare and only detectable in a few tissues. The antigen LST-S3-7 (SEQ ID NO: 63) showed lung and breast tumor specific expression, with its message only being detected in normal testes when the PCR was performed for 30 cycles. Lower level expression was detected in some normal tissues when the cycle number was increased to 35. Antigen LST-S3-13 (SEQ ID NO: 66) was found to be expressed in 3 out of 4 lung tumors, one breast tumor and both colon tumor samples. Its expression in normal tissues was lower compared to tumors, and was only detected in 1 out of 4 normal lung tissues and in normal tissues from kidney, ovary and retina. Expression of antigens LST-S3-4 (SEQ ID NO: 62) and LST-S3-14 (SEQ ID NO: 67) was rare and did not show any tissue or tumor specificity. Consistent with Northern blot analyses, the RT-PCR results on antigen LAT-S1-A-10A (SEQ ID NO: 78) suggested that its expression is high in lung, colon, stomach and small intestine tissues, including lung and colon tumors, whereas its expression was low or undetectable in other tissues.

A total of 2002 cDNA fragments isolated in lung subtractions I, II and III, described above, were colony PCR amplified and their mRNA expression levels in lung tumor, normal lung, and various other normal and tumor tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Seventeen non-redundant cDNA clones showed over-expression in lung squamous tumors, with expression in normal tissues tested (lung, skin, lymph node, colon, liver, pancreas, breast, heart, bone marrow, large intestine, kidney, stomach, brain, small intestine, bladder and salivary gland) being either undetectable, or 10-fold less compared to lung squamous tumors. The determined cDNA sequences for the

clone L513S are provided in SEQ ID NO: 87 and 88; those for L514S are provided in SEQ ID NO: 89 and 90; those for L516S in SEQ ID NO: 91 and 92; that for L517S in SEQ ID NO: 93; that for L519S in SEQ ID NO: 94; those for L520S in SEQ ID NO: 95 and 96; those for L521S in SEQ ID NO: 97 and 98; that for L522S in SEQ ID NO: 99; 5 that for L523S in SEQ ID NO: 100; that for L524S in SEQ ID NO: 101; that for L525S in SEQ ID NO: 102; that for L526S in SEQ ID NO: 103; that for L527S in SEQ ID NO: 104; that for L528S in SEQ ID NO: 105; that for L529S in SEQ ID NO: 106; and those for L530S in SEQ ID NO: 107 and 108. Additionally, the full-length cDNA sequence for L530S is provided in SEQ ID NO: 151, with the corresponding amino acid sequence 10 being provided in SEQ ID NO: 152. L530S shows homology to a splice variant of a p53 tumor suppressor homologue, p63. The cDNA sequences of 7 known isoforms of p63 are provided in SEQ ID NO: 331-337, with the corresponding amino acid sequences being provided in SEQ ID NO: 338-344, respectively.

Due to polymorphisms, the clone L531S appears to have two forms. A 15 first determined full-length cDNA sequence for L531S is provided in SEQ ID NO: 109, with the corresponding amino acid sequence being provided in SEQ ID NO: 110. A second determined full-length cDNA sequence for L531S is provided in SEQ ID NO: 111, with the corresponding amino acid sequence being provided in SEQ ID NO: 112. The sequence of SEQ ID NO: 111 is identical to that of SEQ ID NO: 109, except that it 20 contains a 27 bp insertion. Similarly, L514S has two alternatively spliced forms; the first variant cDNA is listed as SEQ ID NO: 153, with the corresponding amino acid sequence being provided in SEQ ID NO: 155. The full-length cDNA for the second variant form of L514S is provided in SEQ ID NO: 154, with the corresponding amino acid sequence being provided in SEQ ID NO: 156.

25 Full length cloning for L524S (SEQ ID NO: 101) yielded two variants (SEQ ID NO: 163 and 164) with the corresponding amino acid sequences of SEQ ID NO: 165 and 166, respectively. Both variants have been shown to encode parathyroid hormone-related peptide.

Attempts to isolate the full-length cDNA for L519S, resulted in the 30 isolation of the extended cDNA sequence provided in SEQ ID NO: 173, which contains

a potential open reading frame. The amino acid sequence encoded by the sequence of SEQ ID NO: 173 is provided in SEQ ID NO: 174. Additionally, the full-length cDNA sequence for the clone of SEQ ID NO: 100 (known as L523S), a known gene, is provided in SEQ ID NO: 175, with the corresponding amino acid sequence being
5 provided in SEQ ID NO: 176. In further studies, a full-length cDNA sequence for L523S was isolated from a L523S-positive tumor cDNA library by PCR amplification using gene specific primers designed from the sequence of SEQ ID NO: 175. The determined full-length cDNA sequence is provided in SEQ ID NO: 347. The amino acid sequence encoded by this sequence is provided in SEQ ID NO: 348. This protein
10 sequence differs from the previously published protein sequence at two amino acid positions, namely at positions 158 and 410.

Comparison of the sequences of L514S and L531S (SEQ ID NO: 87 and 88, and 109, respectively) with those in the gene bank, as described above, revealed no significant homologies to known sequences. The sequences of L513S, L516S, L517S,
15 L519S, L520S and L530S (SEQ ID NO: 87 and 88, 91 and 92, 93, 94, 95 and 96, 107 and 108, respectively) were found to show some homology to previously identified ESTs. The sequences of L521S, L522S, L523S, L524S, L525S, L526S, L527S, L528S and L529S (SEQ ID NO: 97 and 98, 99, 99, 101, 102, 103, 104, 105, and 106, respectively) were found to represent known genes. The determined full-length cDNA
20 sequence for L520S is provided in SEQ ID NO: 113, with the corresponding amino acid sequence being provided in SEQ ID NO: 114. Subsequent microarray analysis showed L520S to be overexpressed in breast tumors in addition to lung squamous tumors.

Further analysis demonstrated that L529S (SEQ ID NO: 106 and 115),
25 L525S (SEQ ID NO: 102 and 120) and L527S (SEQ ID NO: 104) are cytoskeletal components and potentially squamous cell specific proteins. L529S is connexin 26, a gap junction protein. It was found to be highly expressed in one lung squamous tumor, referred to as 9688T, and moderately over-expressed in two others. However, lower level expression of connexin 26 is also detectable in normal skin, colon, liver and
30 stomach. The over-expression of connexin 26 in some breast tumors has been reported

and a mutated form of L529S may result in over-expression in lung tumors. L525S is plakophilin 1, a desmosomal protein found in plaque-bearing adhering junctions of the skin. Expression levels for L525S mRNA was highly elevated in three out of four lung squamous tumors tested, and in normal skin. L527S has been identified as keratin 6
5 isoform, type II 58 Kd keratin and cytokeratin 13, and shows over-expression in squamous tumors and low expression in normal skin, breast and colon tissues. Keratin and keratin-related genes have been extensively documented as potential markers for lung cancer including CYFRA2.1 (Pastor, A., et al, *Eur. Respir. J.*, 10:603-609, 1997). L513S (SEQ ID NO: 87 and 88) shows moderate over-expression in several tumor
10 tissues tested, and encodes a protein that was first isolated as a pemphigus vulgaris antigen.

L520S (SEQ ID NO: 95 and 96) and L521S (SEQ ID NO: 97 and 98) are highly expressed in lung squamous tumors, with L520S being up-regulated in normal salivary gland and L521S being over-expressed in normal skin. Both belong to a family
15 of small proline rich proteins and represent markers for fully differentiated squamous cells. L521S has been described as a specific marker for lung squamous tumor (Hu, R., et al, *Lung Cancer*, 20:25-30, 1998). L515S (SEQ ID NO: 162) encodes IGF- β 2 and L516S is an aldose reductase homologue. Both are moderately expressed in lung squamous tumors and in normal colon. Notably, L516S (SEQ ID NO: 91 and 92) is up-
20 regulated in metastatic tumors but not primary lung adenocarcinoma, an indication of its potential role in metatasis and a potential prognostic marker. L522S (SEQ ID NO: 99) is moderately over-expressed in lung squamous tumors with minimum expression in normal tissues. L522S has been shown to belong to a class IV alcohol dehydrogenase, ADH7, and its expression profile suggests it is a squamous cell specific antigen. L523S
25 (SEQ ID NO: 100) is moderately over-expressed in lung squamous tumor, human pancreatic cancer cell lines and pancreatic cancer tissues, suggesting this gene may be a shared antigen between pancreatic and lung squamous cell cancer.

L524S (SEQ ID NO: 101) is over-expressed in the majority of squamous tumors tested and is homologous with parathyroid hormone-related peptide (PTHrP),
30 which is best known to cause humoral hypercalcaemia associated with malignant

tumors such as leukemia, prostate and breast cancer. It is also believed that PTHrP is most commonly associated with squamous carcinoma of lung and rarely with lung adenocarcinoma (Davidson, L.A., et al, *J. Pathol.*, 178: 398-401, 1996). L528S (SEQ ID NO: 105) is highly over-expressed in two lung squamous tumors with moderate
5 expression in two other squamous tumors, one lung adenocarcinoma and some normal tissues, including skin, lymph nodes, heart, stomach and lung. It encodes the NMB gene that is similar to the precursor of melanocyte specific gene Pmel17, which is reported to be preferentially expressed in low-metastatic potential melanoma cell lines. This suggests that L528S may be a shared antigen in both melanoma and lung squamous
10 cell carcinoma. L526S (SEQ ID NO: 103) was overexpressed in all lung squamous cell tumor tissues tested and has been shown to share homology with a gene (ATM) in which a mutation causes ataxia telangiectasia, a genetic disorder in humans causing a predisposition to cancer, among other symptoms. ATM encodes a protein that activates a p53 mediated cell-cycle checkpoint through direct binding and phosphorylation of the
15 p53 molecule. Approximately 40% of lung cancers are associated with p53 mutations, and it is speculated that over-expression of ATM is a result of compensation for loss of p53 function, but it is unknown whether over-expression is the cause of result of lung squamous cell carcinoma. Additionally, expression of L526S (ATM) is also detected in a metastatic but not lung adenocarcinoma, suggesting a role in metastasis.

20 Expression of L523S (SEQ ID NO: 175), was examined by real time RT-PCR as described above. In a first study using a panel of lung squamous tumors, L523S was found to be expressed in 4/7 lung squamous tumors, 2/3 head and neck squamous tumors and 2/2 lung adenocarcinomas, with low level expression being observed in skeletal muscle, soft palate and tonsil. In a second study using a lung
25 adenocarcinoma panel, expression of L523S was observed in 4/9 primary adenocarcinomas, 2/2 lung pleural effusions, 1/1 metastatic lung adenocarcinomas and 2/2 lung squamous tumors, with little expression being observed in normal tissues.

Expression of L523S in lung tumors and various normal tissues was also examined by Northern blot analysis, using standard techniques. In a first study, L523S
30 was found to be expressed in a number of lung adenocarcinomas and squamous cell

carcinomas, as well as normal tonsil. No expression was observed in normal lung. In a second study using a normal tissue blot (referred to as HB-12) from Clontech, no expression was observed in brain, skeletal muscle, colon, thymus, spleen, kidney, liver, small intestine, lung or PBMC, although there was strong expression in placenta.

5

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF LUNG TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

Eight hundred and fifty seven clones from a cDNA subtraction library,
10 containing cDNA from a pool of two human lung squamous tumors subtracted against eight normal human tissue cDNAs including lung, PBMC, brain, heart, kidney, liver, pancreas, and skin, (Clontech, Palo Alto, CA) were derived and submitted to a first round of PCR amplification. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments
15 were subcloned into the P7-Adv vector (Clontech, Palo Alto, CA) and transformed into DH5 α *E. coli* (Gibco, BRL). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

One hundred and sixty two positive clones were sequenced. Comparison
20 of the DNA sequences of these clones with those in the EMBL and GenBank databases, as described above, revealed no significant homologies to 13 of these clones, hereinafter referred to as Contigs 13, 16, 17, 19, 22, 24, 29, 47, 49, 56-59. The determined cDNA sequences for these clones are provided in SEQ ID NO: 125, 127-129, 131-133, 142, 144, 148-150, and 157, respectively. Contigs 1, 3-5, 7-10, 12, 11, 15, 20, 31, 33, 38, 39,
25 41, 43, 44, 45, 48, 50, 53, 54 (SEQ ID NO: 115-124, 126, 130, 134-141, 143, 145-147, respectively) were found to show some degree of homology to previously identified DNA sequences. Contig 57 (SEQ ID NO: 149) was found to represent the clone L519S (SEQ ID NO: 94) disclosed in US. Patent Application No. 09/123,912, filed July 27, 1998. To the best of the inventors' knowledge, none of these sequences have been
30 previously shown to be differentially over-expressed in lung tumors.

mRNA expression levels for representative clones in lung tumor tissues, normal lung tissues (n=4), resting PBMC, salivary gland, heart, stomach, lymph nodes, skeletal muscle, soft palate, small intestine, large intestine, bronchial, bladder, tonsil, kidney, esophagus, bone marrow, colon, adrenal gland, pancreas, and skin (all derived
5 from human) were determined by RT-PCR as described above. Expression levels using microarray technology, as described above, were examined in one sample of each tissue type unless otherwise indicated.

Contig 3 (SEQ ID NO: 116) was found to be highly expressed in all head and neck squamous cell tumors tested (17/17), and expressed in the majority (8/12) of
10 lung squamous tumors, (high expression in 7/12, moderate in 2/12, and low in 2/12), while showing negative expression for 2/4 normal lung tissues and low expression in the remaining two samples. Contig 3 showed moderate expression in skin and soft palate, and lowered expression levels in resting PBMC, large intestine, salivary gland, tonsil, pancreas, esophagus, and colon. Contig 11 (SEQ ID NO: 124) was found to be
15 expressed in all head and neck squamous cell tumors tested (17/17), with high levels of expression being seen in 14/17 tumors, and moderately levels of expression being seen in 3/17 tumors. Additionally, high expression was seen in 3/12 lung squamous tumors and moderate expression in 4/12 lung squamous tumors. Contig 11 was negative for 3/4 normal lung samples, with the remaining sample having only low expression. Contig
20 11 showed low to moderate reactivity to salivary gland, soft palate, bladder, tonsil, skin, esophagus, and large intestine. Contig 13 (SEQ ID NO: 125) was found to be expressed in all head and neck squamous cell tumors tested (17/17), with high expression in 12/17, and moderate expression in 5/17. Contig 13 was expressed in 7/12 lung squamous tumors, with high expression in 4/12 and moderate expression in three
25 samples. Analysis of normal lung samples showed negative expression for 2/4 and low to moderate expression in the remaining two samples. Contig 13 showed low to moderate reactivity to resting PBMC, salivary gland, bladder, pancreas, tonsil, skin, esophagus, and large intestine, as well as high expression in soft palate. Subsequent full-length cloning efforts revealed that contig 13 (also known as L761P) maps to the 3'

untranslated region of the hSec10p gene. The full-length sequence for this gene is set forth in SEQ ID NO: 368, and encodes the protein set forth in SEQ ID NO: 369.

Contig 16 (SEQ ID NO: 127) was found to be moderately expressed in several head and neck squamous cell tumors (6/17) and one lung squamous tumor, while showing no expression in any normal lung samples tested. Contig 16 showed low reactivity to resting PBMC, large intestine, skin, salivary gland, and soft palate. Contig 17 (SEQ ID NO: 128) was shown to be expressed in all head and neck squamous cell tumors tested (17/17) (highly expressed in 5/17, and moderately expressed in 12/17). Determination of expression levels in lung squamous tumors showed one tumor sample with high expression and 3/12 with moderate levels. Contig 17 was negative for 2/4 normal lung samples, with the remaining samples having only low expression. Additionally, low level expression was found in esophagus and soft palate. Contig 19 (SEQ ID NO: 129) was found to be expressed in most head and neck squamous cell tumors tested (11/17); with two samples having high expression levels, 6/17 showing moderate expression, and low expression being found in 3/17. Testing in lung squamous tumors revealed only moderate expression in 3/12 samples. Expression levels in 2/4 of normal lung samples were negative, the two other samples having only low expression. Contig 19 showed low expression levels in esophagus, resting PBMC, salivary gland, bladder, soft palate and pancreas.

Contig 22 (SEQ ID NO: 131), was shown to be expressed in most head and neck squamous cell tumors tested (13/17) with high expression in four of these samples, moderate expression in 6/17, and low expression in 3/17. Expression levels in lung squamous tumors were found to be moderate to high for 3/12 tissues tested, with negative expression in two normal lung samples and low expression in two other samples (n=4). Contig 22 showed low expression in skin, salivary gland and soft palate. Similarly, Contig 24 (SEQ ID NO: 132) was found to be expressed in most head and neck squamous cell tumors tested (13/17) with high expression in three of these samples, moderate expression in 6/17, and low expression in 4/17. Expression levels in lung squamous tumors were found to be moderate to high for 3/12 tissues tested, with negative expression for three normal lung samples and low expression in one sample

(n=4). Contig 24 showed low expression in skin, salivary gland and soft palate. Contig 29 (SEQ ID NO: 133) was expressed in nearly all head and neck squamous cell tumors tested (16/17): highly expressed in 4/17, moderately expressed in 11/17, with low expression in one sample. Also, it was moderately expressed in 3/12 lung squamous tumors, while being negative for 2/4 normal lung samples. Contig 29 showed low to moderate expression in large intestine, skin, salivary gland, pancreas, tonsil, heart and soft palate. Contig 47 (SEQ ID NO: 142) was expressed in most head and neck squamous cell tumors tested (12/17): moderate expression in 10/17, and low expression in two samples. In lung squamous tumors, it was highly expressed in one sample and moderately expressed in two others (n=13). Contig 47 was negative for 2/4 normal lung samples, with the remaining two samples having moderate expression. Also, Contig 47 showed moderate expression in large intestine, and pancreas, and low expression in skin, salivary gland, soft palate, stomach, bladder, resting PBMC, and tonsil.

Contig 48 (SEQ ID NO: 143) was expressed in all head and neck squamous cell tumors tested (17/17): highly expressed in 8/17 and moderately expressed in 7/17, with low expression in two samples. Expression levels in lung squamous tumors were high to moderate in three samples (n=13). Contig 48 was negative for one out of four normal lung samples, the remaining showing low or moderate expression. Contig 48 showed moderate expression in soft palate, large intestine, pancreas, and bladder, and low expression in esophagus, salivary gland, resting PBMC, and heart. Contig 49 (SEQ ID NO: 144) was expressed at low to moderate levels in 6/17 head and neck squamous cell tumors tested. Expression levels in lung squamous tumors were moderate in three samples (n=13). Contig 49 was negative for 2/4 normal lung samples, the remaining samples showing low expression. Moderate expression levels in skin, salivary gland, large intestine, pancreas, bladder and resting PBMC were shown, as well as low expression in soft palate, lymph nodes, and tonsil. Contig 56 (SEQ ID NO: 148) was expressed in low to moderate levels in 3/17 head and neck squamous cell tumors tested, and in lung squamous tumors, showing low to moderate levels in three out of thirteen samples. Notably, low expression levels were

detected in one adenocarcinoma lung tumor sample (n=2). Contig 56 was negative for 3/4 normal lung samples, and showed moderate expression levels in only large intestine, and low expression in salivary gland, soft palate, pancreas, bladder, and resting PBMC. Contig 58, also known as L769P, (SEQ ID NO: 150) was expressed at moderate levels
5 in 11/17 head and neck squamous cell tumors tested and low expression in one additional sample. Expression in lung squamous tumors showed low to moderate levels in three out of thirteen samples. Contig 58 was negative for 3/4 normal lung samples, with one sample having low expression. Moderate expression levels in skin, large intestine, and resting PBMC were demonstrated, as well as low expression in salivary
10 gland, soft palate, pancreas, and bladder. Contig 59 (SEQ ID NO: 157) was expressed in some head, neck, and lung squamous tumors. Low level expression of Contig 59 was also detected in salivary gland and large intestine.

The full-length cDNA sequence for Contig 22, also referred to as L763P, is provided in SEQ ID NO: 158, with the corresponding amino acid sequence being
15 provided in SEQ ID NO: 159. Real-time RT-PCR analysis of L763P revealed that it is highly expressed in 3/4 lung squamous tumors as well as 4/4 head and neck squamous tumors, with low level expression being observed in normal brain, skin, soft pallet and trachea. Subsequent database searches revealed that the sequence of SEQ ID NO: 158 contains a mutation, resulting in a frameshift in the corresponding protein sequence. A
20 second cDNA sequence for L763P is provided in SEQ ID NO: 345, with the corresponding amino acid sequence being provided in SEQ ID NO: 346. The sequences of SEQ ID NO: 159 and 346 are identical with the exception of the C-terminal 33 amino acids of SEQ ID NO: 159.

The full-length cDNA sequence incorporating Contigs 17, 19, and 24,
25 referred to as L762P, is provided in SEQ ID NO: 160, with the corresponding amino acid sequence being provided in SEQ ID NO: 161. Further analysis of L762P has determined it to be a type I membrane protein and two additional variants have been sequenced. Variant 1 (SEQ ID NO: 167, with the corresponding amino acid sequence in SEQ ID NO: 169) is an alternatively spliced form of SEQ ID NO: 160 resulting in
30 deletion of 503 nucleotides, as well as deletion of a short segment of the expressed

protein. Variant 2 (SEQ ID NO: 168, with the corresponding amino acid sequence in SEQ ID NO: 170) has a two nucleotide deletion at the 3' coding region in comparison to SEQ ID NO: 160, resulting in a secreted form of the expressed protein. Real-time RT-PCR analysis of L762P revealed that is over-expressed in 3/4 lung squamous tumors and 4/4 head & neck tumors, with low level expression being observed in normal skin, soft pallet and trachea.

An epitope of L762P was identified as having the sequence KPGHWTYTLNNTTHSLQALK (SEQ ID NO: 382), which corresponds to amino acids 571-590 of SEQ ID NO:161.

The full-length cDNA sequence for contig 56 (SEQ ID NO: 148), also referred to as L773P, is provided in SEQ ID NO: 171, with the amino acid sequence in SEQ ID NO: 172. L773P was found to be identical to dihydroxyl dehydrogenase at the 3' portion of the gene, with divergent 5' sequence. As a result, the 69 N-terminal amino acids are unique. The cDNA sequence encoding the 69 N-terminal amino acids is provided in SEQ ID NO: 349, with the N-terminal amino acid sequence being provided in SEQ ID NO: 350. Real-time PCR revealed that L773P is highly expressed in lung squamous tumor and lung adenocarcinoma, with no detectable expression in normal tissues. Subsequent Northern blot analysis of L773P demonstrated that this transcript is differentially over-expressed in squamous tumors and detected at approximately 1.6 Kb in primary lung tumor tissue and approximately 1.3 Kb in primary head and neck tumor tissue.

Subsequent microarray analysis has shown Contig 58, also referred to as L769S (SEQ ID NO: 150), to be overexpressed in breast tumors in addition to lung squamous tumors.

EXAMPLE 4

ISOLATION AND CHARACTERIZATION OF LUNG TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

Seven hundred and sixty clones from a cDNA subtraction library, containing cDNA from a pool of two human lung primary adenocarcinomas subtracted

against a pool of nine normal human tissue cDNAs including skin, colon, lung, esophagus, brain, kidney, spleen, pancreas and liver, (Clontech, Palo Alto, CA) were derived and submitted to a first round of PCR amplification. This library (referred to as ALT-1) was subjected to a second round of PCR amplification, following the
5 manufacturer's protocol. The expression levels of these 760 cDNA clones in lung tumor, normal lung, and various other normal and tumor tissues, were examined using microarray technology (Incyte, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse
10 transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity.. A total of 118 clones, of which 55 were unique, were found to be over-expressed in lung tumor tissue, with expression in normal tissues tested (lung, skin, lymph node, colon,
15 liver, pancreas, breast, heart, bone marrow, large intestine, kidney, stomach, brain, small intestine, bladder and salivary gland) being either undetectable, or at significantly lower levels. One of these clones, having the sequence as provided in SEQ ID NO:420 (clone #19014), shows homology to a previously identified clone, L773P. Clone L773P has the full-length cDNA sequence provided in SEQ ID NO:171 and the amino acid
20 sequence provided in SEQ ID NO:172 The isolation of clone #19014 is also described in co-pending U.S. Patent application 09/285,479, filed April 2, 1999.

EXAMPLE 5

SYNTHESIS OF POLYPEPTIDES

25 Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide.
30 Cleavage of the peptides from the solid support is carried out using the following

cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides are precipitated in cold methyl-t-butyl-ether. The peptide pellets are then dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase
5 HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides are characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

10

EXAMPLE 6

PREPARATION OF ANTIBODIES AGAINST LUNG CANCER ANTIGENS

Polyclonal antibodies against the lung cancer antigens L514S, L528S, L531S, L523 and L773P (SEQ ID NO: 155, 225, 112, 176 and 171, respectively) were prepared as follows.

15

Rabbits were immunized with recombinant protein expressed in and purified from *E. coli* as described below. For the initial immunization, 400 µg of antigen combined with muramyl dipeptide (MDP) was injected subcutaneously (S.C.). Animals were boosted S.C. 4 weeks later with 200 µg of antigen mixed with incomplete Freund's Adjuvant (IFA). Subsequent boosts of 100 µg of antigen mixed with IFA
20 were injected S.C. as necessary to induce high antibody titer responses. Serum bleeds from immunized rabbits were tested for antigen-specific reactivity using ELISA assays with purified protein. Polyclonal antibodies against L514S, L528S, L531S, L523S and L773P were affinity purified from high titer polyclonal sera using purified protein attached to a solid support.

25

Immunohistochemical analysis using polyclonal antibodies against L514S was performed on a panel of 5 lung tumor samples, 5 normal lung tissue samples and normal colon, kidney, liver, brain and bone marrow. Specifically, tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with
30 antibody for 1 hr. HRP-labeled anti-mouse followed by incubation with DAB

chromogen was used to visualize L514S immunoreactivity. L514S was found to be highly expressed in lung tumor tissue with little or no expression being observed in normal lung, brain or bone marrow. Light staining was observed in colon (epithelial crypt cells positive) and kidney (tubules positive). Staining was seen in normal liver but
5 no mRNA has been detected in this tissue making this result suspect.

Using the same procedure, immunohistochemical analysis using polyclonal antibodies against L528S demonstrated staining in lung tumor and normal lung samples, light staining in colon and kidney, and no staining in liver and heart.

Immunohistochemical analysis using polyclonal antibodies against
10 L531S demonstrated staining in lung tumor samples, light membrane staining in most normal lung samples, epithelial staining in colon, tubule staining in kidney, ductal epithelial staining in liver and no staining in heart.

Immunohistochemical analysis using polyclonal antibodies against L523S demonstrated staining in all lung cancer samples tested but no staining in normal
15 lung, kidney, liver, colon, bone marrow or cerebellum.

Generation of polyclonal anti-sera against L762P (SEQ ID NO: 169 and 170) was performed as follows. 400 micrograms of lung antigen was combined with 100 micrograms of muramyl dipeptide (MDP). An equal volume of Incomplete Freund's Adjuvant (IFA) was added and then mixed until an emulsion was formed.
20 Rabbits were injected subcutaneously (S.C.). After four weeks the animals were injected S.C. with 200 micrograms of antigen mixed with an equal volume of IFA. Every four weeks animals were boosted with 100 micrograms of antigen. Seven days following each boost the animal was bled. Sera was generated by incubating the blood at 4°C for 12-24 hours followed by centrifugation.

25 Characterization of polyclonal antisera was carried out as follows. Ninety-six well plates were coated with antigen by incubating with 50 microliters (typically 1 microgram) at 4°C for 20 hrs. 250 microliters of BSA blocking buffer was added to the wells and incubated at room temperature for 2 hrs. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera was diluted in PBS and 50 microliters of
30 diluted sera was added to each well and incubated at room temperature for 30 min.

Plates were washed as described above before addition of 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution and incubation at room temperature for 30 min. Plates were washed as described above and 100µl of TMB Microwell Peroxidase Substrate was added to each well. Following a 15 minute incubation in the dark at room temperature, the colorimetric reaction was stopped with 100µl 1N H₂SO₄ and read immediately at 450 nm. Antisera showed strong reactivity to antigen L762P.

Immunohistochemical analysis using polyclonal antibodies against L762P demonstrated staining in all lung cancer samples tested, some light staining in the bronchiole epithelium of normal lung, tubule staining in kidney, light epithelial staining in colon and no staining in heart or liver.

In order to evaluate L773P protein expression in various tissues, immunohistochemistry (IHC) analysis was performed using an affinity purified L773P polyclonal antibody. Briefly, tissue samples were fixed in formalin solution for 12-24 hrs and embedded in paraffin before being sliced into 8 micron sections. Steam heat induced epitope retrieval (SHIER) in 0.1 M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody was added to each section for 25 minutes at indicated concentrations followed by 25 minute incubation with either anti-rabbit or anti-mouse biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 minute incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase (ABC/HRP) system was used along with DAB chromogen to visualize L773P expression. Slides were counterstained with hematoxylin to visualize cell nuclei. Using this approach, L773P protein was detected in 6/8 lung tumors, 4/6 normal lung samples (very light staining in some cases), 1/1 kidney samples (very light staining), 0/1 heart samples, 1/1 colon samples (very light staining) and 0/1 liver samples.

EXAMPLE 7

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

Immunogenic peptides from the lung cancer antigen L762P (SEQ ID
5 NO: 161) for HLA-A2/K^b-restricted CD8⁺ T cells were identified as follows.

The location of HLA-A2 binding peptides within the lung cancer antigen
L762P (SEQ ID NO: 161) was predicted using a computer program which predicts
peptides sequences likely to be to HLA-A*0201 by fitting to the known peptide
binding motif for HLA-A*0201 (Rupert *et al.* (1993) *Cell* 74:929; Rammensee *et al.*
10 (1995) *Immunogenetics* 41:178-228). A series of 19 synthetic peptides corresponding
to a selected subset of the predicted HLA-A*0201 binding peptides was prepared as
described above.

Mice expressing the transgene for human HLA A2/K^b (provided by Dr L.
Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with the
15 synthetic peptides, as described by Theobald *et al.*, *Proc. Natl. Acad. Sci. USA*
92:11993-11997, 1995, with the following modifications. Mice were immunized with
50µg of L762P peptide and 120µg of an I-A^b binding peptide derived from hepatitis B
virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice
were sacrificed and single cell suspensions prepared. Cells were then resuspended at 7
20 x 10⁶ cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD)
containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL),
non-essential amino acids (Gibco BRL), 2 x 10⁻⁵ M 2-mercaptoethanol, 50U/ml
penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads)
L762P peptide- (5µg/ml) and 10mg/ml B₂-microglobulin- (3 µg/ml) LPS blasts (A2
25 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml
LPS for 3 days). After six days, cells (5 x 10⁵/ml) were restimulated with 2.5 x 10⁶/ml
peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman *et al.*, *Science*
258:815-818, 1992) and 5 x 10⁶/ml irradiated (3000 rads) A2/K^b-transgenic spleen
feeder cells. Cells were cultured in the presence of 10U/ml IL-2. Cells were
30 restimulated on a weekly basis as described, in preparation for cloning the line.

Peptide-specific cell lines were cloned by limiting dilution analysis with irradiated (20,000 rads) L762P peptide-pulsed EL4 A2Kb tumor cells (1×10^4 cells/well) as stimulators and irradiated (3000 rads) A2/K^b-transgenic spleen cells as feeders (5×10^5 cells/well) grown in the presence of 10U/ml IL-2. On day 7, cells were
5 restimulated as before. On day 14, clones that were growing were isolated and maintained in culture.

Cell lines specific for the peptides L762P-87 (SEQ ID NO: 226; corresponding to amino acids 87-95 of SEQ ID NO: 161), L762P-145 (SEQ ID NO: 227; corresponding to amino acids 145-153 of SEQ ID NO: 161), L762P-585 (SEQ ID
10 NO: 228; corresponding to amino acids 585-593 of SEQ ID NO: 161), L762P-425 (SEQ ID NO: 229; corresponding to amino acids 425-433 of SEQ ID NO: 161), L762P(10)-424 (SEQ ID NO: 230; corresponding to amino acids 424-433 of SEQ ID NO: 161) and L762P(10)-458 (SEQ ID NO: 231; corresponding to amino acids 458-467 of SEQ ID NO: 161) demonstrated significantly higher reactivity (as measured by
15 percent specific lysis) against L762P peptide-pulsed EL4-A2/K^b tumor target cells than control peptide-pulsed EL4-A2/K^b tumor target cells.

EXAMPLE 8

IDENTIFICATION OF CD4 IMMUNOGENIC T CELL EPITOPES DERIVED FROM 20 THE LUNG CANCER ANTIGEN L762P

CD4 T cell lines specific for the antigen L762P (SEQ ID NO: 161) were generated as follows.

A series of 28 overlapping peptides were synthesized that spanned approximately 50% of the L762P sequence. For priming, peptides were combined into
25 pools of 4-5 peptides, pulsed at 20 micrograms/ml into dendritic cells for 24 hours. The dendritic cells were then washed and mixed with positively selected CD4+ T cells in 96 well U-bottomed plates. Forty cultures were generated for each peptide pool. Cultures were restimulated weekly with fresh dendritic cells loaded with peptide pools. Following a total of 3 stimulation cycles, cells were rested for an additional week and
30 tested for specificity to antigen presenting cells (APC) pulsed with peptide pools using

interferon-gamma ELISA and proliferation assays. For these assays, adherent monocytes loaded with either the relevant peptide pool or an irrelevant peptide were used as APC. T cell lines that appeared to specifically recognize L762P peptide pools both by cytokine release and proliferation were identified for each pool. Emphasis was placed on identifying T cells with proliferative responses. T cell lines that demonstrated either both L762P-specific cytokine secretion and proliferation, or strong proliferation alone were further expanded to be tested for recognition of individual peptides from the pools, as well as for recognition of recombinant L762P. The source of recombinant L762P was *E. coli*, and the material was partially purified and endotoxin positive.

These studies employed 10 micrograms of individual peptides, 10 or 2 micrograms of an irrelevant peptide, and 2 or 0.5 micrograms of either L762P protein or an irrelevant, equally impure, *E. coli* generated recombinant protein. Significant interferon-gamma production and CD4 T cell proliferation was induced by a number of L762P-derived peptides in each pool. The amino acid sequences for these peptides are provided in SEQ ID NO: 232-251. These peptides correspond to amino acids 661-680, 676-696, 526-545, 874-893, 811-830, 871-891, 856-875, 826-845, 795-815, 736-755, 706-725, 706-725, 691-710, 601-620, 571-590, 556-575, 616-635, 646-665, 631-650, 541-560 and 586-605, respectively, of SEQ ID NO: 161.

CD4 T cell lines that demonstrated specificity for individual L762P-derived peptides were further expanded by stimulation with the relevant peptide at 10 micrograms/ml. Two weeks post-stimulation, T cell lines were tested using both proliferation and IFN-gamma ELISA assays for recognition of the specific peptide. A number of previously identified T cells continued to demonstrate L762P-peptide specific activity. Each of these lines was further expanded on the relevant peptide and, following two weeks of expansion, tested for specific recognition of the L762P-peptide in titration experiments, as well as for recognition of recombinant *E. coli*-derived L762P protein. For these experiments, autologous adherent monocytes were pulsed with either the relevant L762P-derived peptide, an irrelevant mammaglobin-derived peptide, recombinant *E. coli*-derived L762P (approx. 50% pure), or an irrelevant *E. coli*-derived protein. The majority of T cell lines were found to show low affinity for the relevant

peptide, since specific proliferation and IFN-gamma ratios dramatically decreased as L762P peptide was diluted. However, four lines were identified that demonstrated significant activity even at 0.1 micrograms/ml peptide. Each of these lines (referred to as A/D5, D/F5, E/A7 and E/B6) also appeared to specifically proliferate in response to the *E. coli*-derived L762P protein preparation, but not in response to the irrelevant protein preparation. The amino acid sequences of the L762P-derived peptides recognized by these lines are provided in SEQ ID NO: 234, 249, 236 and 245, respectively. No protein specific IFN-gamma was detected for any of the lines. Lines A/D5, E/A7 and E/B6 were cloned on autologous adherent monocytes pulsed with the relevant peptide at 0.1 (A/D5 and E/A7) or 1 (D/F5) microgram/ml. Following growth, clones were tested for specificity for the relevant peptide. Numerous clones specific for the relevant peptide were identified for lines A/D5 and E/A7.

EXAMPLE 9

PROTEIN EXPRESSION OF LUNG TUMOR-SPECIFIC ANTIGENS

a) Expression of L514S in *E. coli*

The lung tumor antigen L514S (SEQ ID NO: 89) was subcloned into the expression vector pE32b at NcoI and NotI sites, and transformed into *E. coli* using standard techniques. The protein was expressed from residues 3-153 of SEQ ID NO: 89. The expressed amino acid sequence and the corresponding DNA sequence are provided in SEQ ID NO: 252 and 253, respectively.

b) Expression of L762P

Amino acids 32-944 of the lung tumor antigen L762P (SEQ ID NO: 161), with a 6X His Tag, were subcloned into a modified pET28 expression vector, using kanamycin resistance, and transformed into BL21 CodonPlus using standard techniques. Low to moderate levels of expression were observed. The determined DNA sequence of the L762P expression construct is provided in SEQ ID NO: 254.

EXAMPLE 10

IDENTIFICATION OF MHC CLASS II RESTRICTING ALLELE FOR L762P
PEPTIDE-SPECIFIC RESPONSES

- 5 A panel of HLA mismatched antigen presenting cells (APC) were used to identify the MHC class II restricting allele for the L762P-peptide specific responses of CD4 T cell clones derived from lines that recognized L762P peptide and recombinant protein. Clones from two lines, AD-5 and EA-7, were tested as described below. The AD-5 derived clones were found to be restricted by the HLA-DRB-1101 allele, and an
- 10 EA-7 derived clone was found to be restricted by the HLA DRB-0701 or DQB1-0202 allele. Identification of the restriction allele allows targeting of vaccine therapies using the defined peptide to individuals that express the relevant class II allele. Knowing the relevant restricting allele will also enable clinical monitoring for responses to the defined peptide since only individuals that express the relevant allele will be monitored.
- 15 CD4 T cell clones derived from line AD-5 and EA-7 were stimulated on autologous APC pulsed with the specific peptide at 10 µg/ml, and tested for recognition of autologous APC (from donor D72) as well as against a panel of APC partially matched with D72 at class II alleles. Table 2 shows the HLA class typing of the APC tested. Adherent monocytes (generated by 2 hour adherence) from four different
- 20 donors, referred to as D45, D187, D208, and D326, were used as APC in these experiments. Autologous APC were not included in the experiment. Each of the APC were pulsed with the relevant peptide (5a for AD-5 and 3e for 3A-7) or the irrelevant mammoglobin peptide at 10 µg/ml, and cultures were established for 10,000 T cells and about 20,000 APC/well. As shown in Table 3, specific proliferation and cytokine
- 25 production could be detected only when partially matched donor cells were used as APC. Based on the MHC typing analysis, these results strongly suggest that the restricting allele for the L762-specific response of the AD-5 derived clones is HLA-DRB-1101 and for the EA-7 derived clone the restricting allele is HLA DRB-0701 or DQB1-0202.

Table 2 - HLA Typing of APC

DONOR	DR	DR	DQ	DQ
D72	B1-1101	B1-0701	B1-0202	B1-0301
D45	-3	-15	B1-0201	B1-0602
D187	-4	-15	-1	-7
D208	B1-1101	B1-0407	-3	-3
D326	B1-0301	B1-0701	B1-0202	B1-0201

Table 3 - L762P Peptide Responses Map to HLA DR Alleles

AD-5																														EA-7		
A11			B10			C10			C11			E6			F1			F9			G8			G9			G10			G12		
Prol	γ-IFN		Prol	γ-IFN		Prol	γ-IFN		Prol	γ-IFN		Prol	γ-IFN		Prol	γ-IFN		Prol	γ-IFN		Prol	γ-IFN		Prol	γ-IFN		Prol	γ-IFN				
Donor																																
D72 DR-0701, -1101, DQ-0202, -7	46		31			34			24			31			40			55			45			43			91		10			
D45 DR-3,-15, DQ-1, -0201	32	1.7	5.5	1.2		33	1		1.0	1.5		1.1	1.1		1.6	1.1		1.4	1.3		0.2	1.1		1.1	1.1		1.2	1.5	0.8	1.1		
D187 DR-4, -15, DQ-1,-7	14	1.2	1.3	1		14	1.1		1.4	1.7		1.0	1.1		1.4	1.2		1.2	1.1		0.9	1		1.0	1		1.0	1.6	0.5	1		
D208 DR-4, -1101, DQ-3	138	13	38	5.4		188	10		14.6	4.6		153	6.1		45.9	8.6		733	14.1		38.0	7.7		1743	16.1		113.6	19.6	0.8	1		
D326 DR-3, -0701, DQ-0202	0.7	4	0.3	1		0.3	1.4		1.0	2		0.8	1.1		0.3	1.1		0.7	1.1		0.6	1.2		0.4	1		1.2	5	14.1	6.8		

EXAMPLE 11

FUSION PROTEINS OF N-TERMINAL AND C-TERMINAL PORTIONS OF L763P

In another embodiment, a *Mycobacterium tuberculosis*-derived polynucleotide, referred to as Ra12, is linked to at least an immunogenic portion of a polynucleotide of this invention. Ra12 compositions and methods for their use in enhancing expression of heterologous polynucleotide sequences are described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; see also, Skeiky *et al.*, *Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference). Surprisingly, it was discovered that a 14 KD C-terminal fragment of the MTB32A coding sequence expresses at high levels on its own and remains as a soluble protein throughout the purification process. Moreover, this fragment may enhance the immunogenicity of heterologous antigenic polypeptides with which it is fused. This 14 KD C-terminal fragment of the MTB32A is referred to herein as Ra12 and represents a fragment comprising some or all of amino acid residues 192 to 323 of MTB32A.

Recombinant nucleic acids which encode a fusion polypeptide comprising a Ra12 polypeptide and a heterologous lung tumor polypeptide of interest, can be readily constructed by conventional genetic engineering techniques. Recombinant nucleic acids are constructed so that, preferably, a Ra12 polynucleotide sequence is located 5' to a selected heterologous lung tumor polynucleotide sequence. It may also be appropriate to place a Ra12 polynucleotide sequence 3' to a selected heterologous polynucleotide sequence or to insert a heterologous polynucleotide sequence into a site within a Ra12 polynucleotide sequence.

In addition, any suitable polynucleotide that encodes a Ra12 or a portion or other variant thereof can be used in constructing recombinant fusion polynucleotides comprising Ra12 and one or more lung tumor polynucleotides disclosed herein.

Preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide.

5 Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a
10 fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

Two specific embodiments of fusions between Ra12 and antigens of the
15 present invention are described in this example.

A. N-Terminal Portion of L763P

A fusion protein of full-length Ra12 and the N-terminal portion of L763P (referred to as L763P-N; amino acid residues 1-130 of SEQ ID NO: 159) was expressed as a single recombinant protein in *E. coli*. The cDNA for the N-terminal portion was obtained by
20 PCR with a cDNA for the full length L763P and primers L763F3 (5' CGGCGAATTCATGGATTGGGGGACGCTGC; SEQ ID NO: 383) and 1763RV3 (5' CGGCCTCGAGTCACCCCTCTATCCGAACCTTCTGC; SEQ ID NO: 384). The PCR product with expected size was recovered from agarose gel, digested with restriction enzymes *EcoRI* and *XhoI*, and cloned into the corresponding sites in the
25 expression vector pCRX1. The sequence for the fusion of full-length of Ra12 and L763P-N was confirmed by DNA sequencing. The determined cDNA sequence is provided in SEQ ID NO:351, with the corresponding amino acid sequence being provided in SEQ ID NO: 352).

B. C-Terminal Portion of L763P

A fusion protein of full-length Ra12 and the C-terminal portion of L763P (referred to as L763P-C; amino acid residues 100-262 of SEQ ID NO: 159) was expressed as a single recombinant protein in *E. coli*. The cDNA of the C-terminal
 5 portion of L763P was obtained by PCR with a cDNA for the full length of L763P and primers L763F4 (5' CGGCGAATTCCACGAACCACTCGCAAGTTCAG; SEQ ID NO: 385) and L763RV4 (5' CGGCTCGAG-TTAGCTTGGGCCTGTGATTGC; SEQ ID NO: 386). The PCR product with expected size was recovered from agarose gel, digested with restriction enzymes EcoRI and XhoI, and cloned into the corresponding
 10 sites in the expression vector pCRX1. The sequence for the fusion of full-length Ra12 and L763P-C was confirmed by DNA sequencing. The determined DNA sequence is provided in SEQ ID NO:353, with the corresponding amino acid sequence being provided in SEQ ID NO: 354.

The recombinant proteins described in this example are useful for the
 15 preparation of vaccines, for antibody therapeutics, and for diagnosis of lung tumors.

EXAMPLE 12

EXPRESSION IN *E. COLI* OF L762P HIS TAG FUSION PROTEIN

20 PCR was performed on the L762P coding region with the following primers:

Forward primer starting at amino acid 32.

PDM-278 . 5'ggagtacagcttcaagacaatggg 3' (SEQ ID NO:355) Tm 57°C.

Reverse primer including natural stop codon after amino acid 920,
 25 creating EcoRI site

PDM-280 5'ccatgggaattcattataataattttgttcc 3' (SEQ ID NO:356)
 TM55°C.

The PCR product was digested with EcoRI restriction enzyme, gel purified and then cloned into pPDM His, a modified pET28 vector with a His tag in
 30 frame, which had been digested with Eco72I and EcoRI restriction enzymes. The

correct construct was confirmed by DNA sequence analysis and then transformed into BL21 (DE3) pLys S and BL21 (DE3) CodonPlus RIL expression hosts.

The protein sequence of expressed recombinant L762P is shown in SEQ ID NO:357, and the DNA sequence is shown in SEQ ID NO:358.

5

EXAMPLE 13

EXPRESSION IN *E. COLI* OF A L773PA HIS TAG FUSION PROTEIN

The L773PA coding region (encoding amino acids 2-71 of SEQ ID NO: 10 172) was PCR amplified using the following primers:

Forward primer for L773PA starting at amino acid 2:

PDM-299 5'tggcagccctcttctcaagtggc 3' (SEQ ID NO:359) Tm63°C.

Reverse primer for L773PA creating artificial stop codon after amino acid 70:

15 PDM-355 5'cgccagaattcatcaacaaatctgtagcacc 3' (SEQ ID NO:360)
Tm62°C.

The resulting PCR product was digested with EcoRI restriction enzyme, gel purified and then cloned into pPDM His, a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The 20 correct construct was confirmed by DNA sequence analysis and transformed into BL21 (DE3) pLys S and BL21 (DE3) CodonPlus RIL expression hosts.

The protein sequence of expressed recombinant L773PA is shown in SEQ ID NO:361, and the DNA sequence is shown in SEQ ID NO:362.

25

EXAMPLE 14

IDENTIFICATION OF EPITOPES DERIVED FROM LUNG TUMOR SPECIFIC POLYPEPTIDES

A series of peptides from the L773P amino acid sequence (SEQ ID NO: 30 172) were synthesized and used in *in vitro* priming experiments to generate peptide-specific CD4 T cells. These peptides were 20-mers that overlapped by 15 amino acids

and corresponded to amino acids 1-69 of the L773P protein. This region has been demonstrated to be tumor-specific. Following three *in vitro* stimulations, CD4 T cell lines were identified that produced IFN γ in response to the stimulating peptide but not the control peptide. Some of these T cell lines demonstrated recognition of recombinant L773P and L773PA (tumor-specific region) proteins.

To perform the experiments, a total of eleven 20-mer peptides (SEQ ID NOs: 363, 365 and 387-395) overlapping by 15 amino acids and derived from the N-terminal tumor-specific region of L773P (corresponding to amino acids 1-69 of SEQ ID NO:172) were generated by standard procedures. Dendritic cells were derived from PBMC of a normal donor using GMCSF and IL-4 by standard protocol. Purified CD4 T cells were generated from the same donor as the dendritic cells using MACS beads and negative selection of PBMCs. Dendritic cells were pulsed overnight with the individual 20-mer peptides at a concentration of 10 μ g/ml. Pulsed dendritic cells were washed and plated at 1×10^4 /well of a 96-well U-bottom plates, and purified CD4 cells were added at 1×10^5 well. Cultures were supplemented with 10 ng/ml IL-6 and 5 ng/ml IL-12, and incubated at 37°C. Cultures were re-stimulated as above on a weekly basis using as APC dendritic cells generated and pulsed as above, supplemented with 5 ng/ml IL-7 and 10 μ g/ml IL-2. Following 3 *in vitro* stimulation cycles, cell lines (each corresponding to one well) were tested for cytokine production in response to the stimulating peptide vs. an irrelevant peptide.

A small number of individual CD4 T cell lines (9/528) demonstrated cytokine release (IFN γ) in response to the stimulating peptide but not to control peptide. The CD4 T cell lines that demonstrated specific activity were restimulated on the appropriate L773P peptide and reassayed using autologous dendritic cells pulsed with 10 μ g/ml of the appropriate L773P peptide, an irrelevant control peptide, recombinant L773P protein (amino acids 2-364, made in *E. coli*), recombinant L773PA (amino acids 2-71, made in *E. coli*), or an appropriate control protein (L3E, made in *E. coli*). Three of the nine lines tested (1-3C, 1-6G, and 4-12B) recognized the appropriate L773P peptide as well as recombinant L773P and L773PA. Four of the lines tested (4-8A, 4-8E, 4-12D, and 4-12E) recognized the appropriate L773P peptide only. Two of the lines tested (5-6F and 9-3B) demonstrated non-specific activity.

These results demonstrate that the peptide sequences MWQPLFFKWLLSCCPGSSQI (amino acids 1-20 of SEQ ID NO: 172; SEQ ID NO:363) and GSSQIAAAASTQPEDDINTQ (amino acids 16-35 of SEQ ID NO: 172; SEQ ID NO: 365) may represent naturally processed epitopes of L773P, which are
5 capable of stimulating human class II MHC-restricted CD4 T cell responses.

In subsequent studies, the above epitope mapping experiment was repeated using a different donor. Again, some of the resulting T cell lines were found to respond to peptide and recombinant protein. An additional peptide was found to be naturally processed. Specifically, purified CD4 cells were stimulated on a total of
10 eleven 20-mer peptides overlapping by 15 amino acids (SEQ ID NO: 363, 387, 388, 365 and 389-395, respectively). The priming was carried out as described above, except that a peptide concentration of 0.5 ug/mL rather than 10 ug/mL was employed. In the initial screen of the cell lines 9 of the 528 lines released at least a three-fold greater level of IFN-gamma with stimulating peptide vs. control peptide. These 9 lines were
15 restimulated on the appropriate peptide and then tested on dendritic cells pulsed with a titration of appropriate peptide (10 ug/mL, 1 ug/mL and 0.1 ug/mL), and 10 ug/mL of a control peptide. Six of the 9 lines recognized recombinant L773P as well as peptide. The six lines referred to as 1-1E, 1-2E, 1-4H, 1-6A, 1-6G and 2-12B recognized L773PA and the appropriate peptide. These results demonstrate that the peptides of
20 SEQ ID NO: 363 and 387 represent naturally processed epitopes of L773P.

Using the procedures described above, CD4+ T cell responses were generated from PBMC of normal donors using dendritic cells pulsed with overlapping 20-mer peptides (SEQ ID NO: 396-419) spanning the L523S polypeptide sequence (SEQ ID NO: 176). A number of CD4+ T cells demonstrated reactivity with the
25 priming peptides as well as with L523S recombinant protein, with the dominant reactivity of these lines being within the peptides 4, 7 and 21 (SEQ ID NO: 399, 402 and 416; corresponding to amino acids 30-39, 60-79 and 200-219, respectively, of SEQ ID NO: 176).

Epitopes within the scope of the invention include epitopes restricted by
30 other class II MHC molecules. In addition, variants of the peptide can be produced wherein one or more amino acids are altered such that there is no effect on the ability of

the peptides to bind to MHC molecules, no effect on their ability to elicit T cell responses, and no effect on the ability of the elicited T cells to recognize recombinant protein.

5

EXAMPLE 15

SURFACE EXPRESSION OF L762P AND
ANTIBODY EPITOPES THEREOF

Rabbits were immunized with full-length histidine-tagged L762P protein
10 generated in *E. coli*. Sera was isolated from rabbits and screened for specific
recognition of L762P in ELISA assays. One polyclonal serum, referred to as 2692L, was
identified that specifically recognized recombinant L762P protein. The 2692L anti-
L762P polyclonal antibodies were purified from the serum by affinity purification using
L762P affinity columns. Although L762P is expressed in a subset of primary lung tumor
15 samples, expression appears to be lost in established lung tumor cell lines. Therefore,
to characterize surface expression of L762P, a retrovirus construct that expresses L762P
was used to transduce primary human fibroblasts as well as 3 lung tumor cell lines (522-
23, HTB, and 343T). Transduced lines were selected and expanded to examine L762P
surface expression by FACS analysis. For this analysis, non-transduced and transduced
20 cells were harvested using cell dissociation medium, and incubated with 10-50
micrograms/ml of either affinity purified anti-L762P or irrelevant antisera. Following a
30 minute incubation on ice, cells were washed and incubated with a secondary, FITC
conjugated, anti rabbit IgG antibody as above. Cells were washed, resuspended in buffer
with Propidium Iodide (PI) and examined by FACS using an Excalibur fluorescence
25 activated cell sorter. For FACS analysis, PI-positive (i.e. dead/permeabilized cells) were
excluded. The polyclonal anti-L762P sera specifically recognized and bound to the
surface of L762P-transduced cells but not the non-transduced counterparts. These
results demonstrate that L762P is localized to the cell surface of both fibroblasts as well
as lung tumor cells.

30

To identify the peptide epitopes recognized by 2692L, an epitope
mapping approach was pursued. A series of overlapping 19-21 mers (5 amino acid

overlap) was synthesized that spanned the C terminal portion of L762P (amino acids 481-894 of SEQ ID NO: 161). In an initial experiment peptides were tested in pools. Specific reactivity with the L762P antiserum was observed with pools A, B, C, and E. To identify the specific peptides recognized by the antiserum, flat bottom 96 well
5 microtiter plates were coated with individual peptides at 10 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 5% (w/v) milk for 2 hours at 37 °C, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit anti-L762P serum 2692L was added at 200 or 20 ng/well to triplicate wells in PBST and incubated overnight at room temperature. This
10 was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti rabbit IgG (H+L)Affinipure F(ab') fragment at 1:2,000 for 60 minutes. Plates were then washed, and incubated in tetramethyl benzidine substrate. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450/570 nm using an ELISA plate reader.

15 The resulting data, presented in Table 4 below, demonstrates that the L762P antisera recognized at least 6 distinct peptide epitopes from the 3' half of L762P.

Table 4

Peptide (starting amino acid of L762P)	pool	ELISA activity (OD 450-570)	
		200 ng polyclonal serum	20 ng polyclonal serum
A (481)	A	1.76	1.0
B (495)	A	0.14	0.06
C (511)	E	0.47	0.18
D (526)	E	0.11	0.09
E (541)	A	0.11	0.04
F (556)	A	0.04	0.02
G (571)	A	0.06	0.02
H (586)	B	0.1	0.03
I (601)	B	0.25	0.06
J (616)	B	0.1	0.03
K (631)	E	0.1	0.08
L (646)	B	0.28	0.12
M (661)	B	0.14	0.03
N (676)	C	0.12	0.1
O (691)	C	1.1	0.23
P (706)	C	0.1	0.03
Q (721)	C	0.11	0.05
R (736)	E	0.12	0.04
S (751)	C	0.15	0.06
U (781)	D	0.12	0.06
V (795)	F	0.07	0.05
X (826)	D	0.1	0.03
Y (841)	D	0.17	0.07
Z (856)	D	0.16	0.08
AA (871)	F	0.17	0.05
BB (874)	F	0.14	0.11
No peptide		0.15	0.045

Individual peptides were identified from each of the pools, and additionally a weak reactivity was identified with peptide BB from pool F. The relevant peptide epitopes are summarized in the Table 5 below. The amino acid sequences for peptides BB, O, L, I, A and C are provided in SEQ ID NO: 376-381, respectively, with the corresponding cDNA sequences being provided in SEQ ID NO: 373, 370, 372, 374, 371 and 375, respectively.

Table 5

Peptide	Nucleotides of L762P	Amino acids of L762P	Sequence	pool	ELISA activity (OD 450-570)	
					200 ng	20 ng
A	1441-1500	481-500	SRISSGTGDIFQQHIQLEST	A	1.76	1.0
C	1531-1590	511-530	KNTVTVDNTVGNDTMFLVTW	E	0.47	0.18
I	1801-1860	601-620	AVPPATVEAFVERDSLHFPH	B	0.25	0.06
L	1936-1955	646-665	PETGDPVTLRLDDGAGADV	B	0.28	0.12
O	2071-2130	691-710	VNHSPSISTPAHSIPGSHAMIL	C	1.1	0.23
BB	2620-2679	874-893	LQSAVSANIAQAPLFIPPNSD	F	0.14	0.11
None	-	-	-	-	0.15	0.05

EXAMPLE 16

5 DETECTION OF ANTIBODIES AGAINST LUNG TUMOR ANTIGENS
IN PATIENT SERA

Antibodies specific for the lung tumor antigens L773PA (SEQ ID NO:361), L514S (SEQ ID NO:155 and 156), L523S (SEQ ID NO:176), L762P (SEQ ID NO:161) and L763P (SEQ ID NO:159) were shown to be present in effusion fluid or sera of lung cancer patients but not in normal donors. More specifically, the presence of antibodies against L773PA, L514S, L523S, L762P and L763P in effusion fluid obtained from lung cancer patients and in sera from normal donors was detected by ELISA using recombinant proteins and HRP-conjugated anti-human Ig. Briefly, each protein (100 ng) was coated in 96-well plate at pH 9.5. In parallel, BSA (bovine serum albumin) was also coated as a control protein. The signals ([S], absorbance measured at 405 nm) against BSA ([N]) were determined. The results of these studies are shown in Table 6, wherein - represents $[S]/[N] < 2$; +/- represents $[S]/[N] > 2$; ++ represents $[S]/[N] > 3$; and +++ represents $[S]/[N] > 5$.

20

Table 6 – Detection of Antibodies against Lung Tumor Antigens

Effusion fluid	L514S	L523S	L762P	L763P	L773PA
#1	+++	++	++	-	++
#2	-	-	+/-	++	+/-
#3	-	-	-	-	+/-
#4	+/-	++	+/-	-	+/-
#5	+/-	+++	+/-	+/-	++
#7	-	+/-	-	-	+/-
#8	-	+++	-	-	++
#10	-	++	+/-	+/-	-
#11	+/-	++	++	-	++
#12	+++	+/-	-	+/-	+/-
#13	-	+/-	-	-	+/-
#14	-	+++	+/-	+/-	++
#15	+/-	++	+/-	-	++
#17	-	+/-	-	-	+/-
#18	-	++	-	-	-
#19	-	+/-	-	-	+/-
#20	+/-	+/-	+/-	-	+/-
Normal sera					
#21	-	+/-	-	-	-
#22	-	-	-	-	-
#23	-	-	-	-	-
#24	-	+/-	-	-	+/-
#25	+/-	+/-	-	-	+/-

Using Western blot analyses, antibodies against L523S were found to be present in 3 out of 4 samples of effusion fluid from lung cancer patients, with no L523S antibodies being detected in the three samples of normal sera tested.

EXAMPLE 17

EXPRESSION IN *E. COLI* OF A L514S HIS TAG FUSION PROTEIN

PCR was performed on the L514S-13160 coding region with the following primers:

Forward primer PDM-278 5' cacactagtgtccgcgtggcgccctac 3' (SEQ ID NO:421) Tm 67°C.

Reverse primer PDM-280 5' catgagaattcatcacatgcccttgaaggctccc 3' (SEQ ID NO:422) TM 66°C.

5 The PCR conditions were as follows:

10µl 10X Pfu buffer

1.0µl 10mM dNTPs

2.0µl 10µM each primer

83µl sterile water

10 1.5µl Pfu DNA polymerase (Stratagene, La Jolla, CA)

50ng DNA

96°C for 2 minutes, 96°C for 20 seconds, 66°C for 15 seconds, 72°C for 1 minute with 40 cycles and then 72°C for 4 minutes.

The PCR product was digested with EcoRI restriction enzyme, gel
15 purified and then cloned into pPDM His, a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into BL21 CodonPlus (Stratagene, La Jolla, CA) cells for expression.

The amino acid sequence of expressed recombinant L514S is shown in
20 SEQ ID NO:423, and the DNA coding region sequence is shown in SEQ ID NO:424.

EXAMPLE 18

EXPRESSION IN *E. COLI* OF A L523S HIS TAG FUSION PROTEIN

25 PCR was performed on the L523S coding region with the following primers:

Forward primer PDM-414 5' aacaaactgtatatcggaaacctcagcgagaa 3' (SEQ ID NO:425) Tm 62°C.

Reverse primer PDM-415 5' ccatagaattcattactccgtcttgactgagg 3' (SEQ
30 ID NO:426) TM 62°C.

The PCR conditions were as follows:

10µl 10X Pfu buffer

1.0µl 10mM dNTPs

2.0µl 10µM each primer

83µl sterile water

1.5µl Pfu DNA polymerase (Stratagene, La Jolla, CA)

50ng DNA

96°C for 2 minutes, 96°C for 20 seconds, 62°C for 15 seconds, 72°C for 4 minutes with 40 cycles and then 72°C for 4 minutes.

The PCR product was digested with EcoRI restriction enzyme, gel purified and then cloned into pPDM His, a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into BL21 CodonPlus (Stratagene, La Jolla, CA) cells for expression.

The amino acid sequence of expressed recombinant L523S is shown in SEQ ID NO:427, and the DNA coding region sequence is shown in SEQ ID NO:428.

EXAMPLE 19

EXPRESSION IN *E. COLI* OF A L762PA HIS TAG FUSION PROTEIN

PCR was performed on the L762PA coding region (L762PA is missing the signal sequence, the C-terminal transmembrane domain and the cytoplasmic tail) with the following primers:

Forward primer PDM-278 5'ggagtacagcttcaagacaatggg 3' (SEQ ID NO:355) Tm 57°C.

Reverse primer PDM-279 5'ccatggaattcattatttcaatataagataatctc 3' (SEQ ID NO:429) TM56°C.

The PCR conditions were as follows:

10µl 10X Pfu buffer

1.0µl 10mM dNTPs

2.0µl 10µM each primer
 83µl sterile water
 1.5µl Pfu DNA polymerase (Stratagene, La Jolla, CA)
 50ng DNA

5 96°C for 2 minutes, 96°C for 20 seconds, 55°C for 15 seconds, 72°C for
 5 minutes with 40 cycles and then 72°C for 4 minutes.

The PCR product was digested with EcoRI restriction enzyme, gel
 purified and then cloned into pPDM His, a modified pET28 vector with a His tag in
 frame, which had been digested with Eco72I and EcoRI restriction enzymes. The
 10 correct construct was confirmed by DNA sequence analysis and then transformed into
 BL21 pLys S (Novagen, Madison, WI) cells for expression.

The amino acid sequence of expressed recombinant L762PA is shown in
 SEQ ID NO:430, and the DNA coding region sequence is shown in SEQ ID NO:431.

15

EXAMPLE 20

EXPRESSION IN *E. COLI* OF A L773P HIS TAG FUSION PROTEIN

PCR was performed on the L773P coding region with the following
 primers:

20 Forward primer PDM-299 5' tggcagcccctcttcttcaagtggc 3' (SEQ ID
 NO:359) Tm 63°C.

Reverse primer PDM-300 5' cgctgctcgagtcattaatattcatcagaaaatgg 3'
 (SEQ ID NO:432) TM 63°C.

The PCR conditions were as follows:

25 10µl 10X Pfu buffer
 1.0µl 10mM dNTPs
 2.0µl 10µM each primer
 83µl sterile water
 1.5µl Pfu DNA polymerase (Stratagene, La Jolla, CA)
 30 50ng DNA

96°C for 2 minutes, 96°C for 20 seconds, 63°C for 15 seconds, 72°C for 2 minutes 15 seconds with 40 cycles and then 72°C for 4 minutes.

The PCR product was digested with EcoRI restriction enzyme, gel purified and then cloned into pPDM His, a modified pET28 vector with a His tag in frame, which had been digested with Eco2I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into BL21 pLys S (Novagen, Madison, WI) and BL21 CodonPlus (Stratagene, La Jolla, CA) cells for expression.

The amino acid sequence of expressed recombinant L773P is shown in SEQ ID NO:433, and the DNA coding region sequence is shown in SEQ ID NO:434.

EXAMPLE 21

CLONING AND SEQUENCING OF A T-CELL RECEPTOR CLONE FOR THE LUNG SPECIFIC ANTIGEN L762P

T cell receptor (TCR) alpha and beta chains from a CD4 T cell clone specific for the lung specific antigen L762P were cloned and sequence. Basically, total mRNA from 2×10^6 cells from CTL clone 4H6 was isolated using Trizol reagent and cDNA was synthesized using Ready-to go kits (Pharmacia). To determine Valpha and Vbeta sequences of this clone, a panel of Valpha and Vbeta subtype specific primers was synthesized and used in RT-PCR reactions with cDNA generated from each of the clones. The RT-PCR reactions demonstrated that each of the clones expressed a common Vbeta sequence that corresponded to the Vbeta8 subfamily and a Valpha sequence that corresponded to the Valpha8 subfamily. To clone the full TCR alpha and beta chains from clone 4H6, primers were designed that spanned the initiator and terminator-coding TCR nucleotides. The primers were as follows:

forward primer for TCR Valpha8 5'
ggatccgccgccaccatgacatccattcgagctgta 3' (SEQ ID NO:435; has a BamHI site inserted);

Kozak reverse primer for TCR Valpha8 (antisense) 5' gtcgactcagctggaccacagccgcag 3' (SEQ ID NO:436; has a Sall site inserted plus the TCR alpha constant sequence);

forward primer for TCR Vbeta8 (sense) 5' ggatccgccgccaccatggactcctggaccttctgct 3' (SEQ ID NO:437; has a BamHI site inserted); and

Kozak reverse primer for TCR Vbeta 5' gtcgactcagaaatcctttctgtgac 3' (SEQ ID NO:438; has a Sall site inserted plus the TCR beta constant sequence).

Standard 35 cycle RT-PCR reactions were established using the cDNA synthesized from the CTL clone and the above primers utilizing the proofreading thermostable polymerase, PWO (Roche). The resultant PCR band, about 850 bp for Valpha and about 950 for Vbeta, was ligated into a PCR blunt vector (Invitrogen) and transformed into *E. coli*. *E. coli* transformed with plasmids having full-length alpha and beta chains were identified.. Large scale preparations of the corresponding plasmids were generated, and these plasmids were sequenced. The Valpha sequence (SEQ ID NO:439) was shown by nucleotide sequence alignment to be homologous to Valpha8.1, while the Vbeta sequence (SEQ ID NO:440) was shown by nucleotide sequence alignment to be homologous to Vbeta8.2.

20

EXAMPLE 22

RECOMBINANT EXPRESSION OF FULL LENGTH L762P IN MAMMALIAN CELLS

Full length L762P cDNA was subcloned into the mammalian expression vectors VR1012 and pCEP4 (Invitrogen). Both expression vectors had previously been modified to contain a FLAG epitope tag. These constructs were transfected into HEK293 and CHL-1 cells (ATCC) using Lipofectamine 2000 reagent (Gibco). Briefly, both the HEK and CHL-1 cells were plated at a density of 100,000 cells/ml in DMEM (Gibco) containing 10% FBS (Hyclone) and grown overnight. The following day, 4μl of Lipofectamine 2000 was added to 100μl of DMEM containing no FBS and incubated

30

for 5 minutes at room temperature. The Lipofectamine/DMEM mixture was then added to 1µg of L762P Flag/pCEP4 or L762P Flag/VR1012 plasmid DNA resuspended in 100µl DMEM and incubated for 15 minutes at room temperature. The Lipofectamine/DNA mix was then added to the HEK293 and CHL-1 cells and
5 incubated for 48-72 hours at 37°C with 7% CO₂. Cells were rinsed with PBS, then collected and pelleted by centrifugation. L762P expression was detected in the transfected HEK293 and CHL-1 cell lysates by Western blot analysis and was detected on the surface of transfected HEK cells by flow cytometry analysis.

For Western blot analysis, whole cell lysates were generated by
10 incubating the cells in Triton-X100 containing lysis buffer for 30 minutes on ice. Lysates were then cleared by centrifugation at 10,000 rpm for 5 minutes at 4°C. Samples were diluted with SDS-PAGE loading buffer containing beta-mercaptoethanol, then boiled for 10 minutes prior to loading the SDS-PAGE gel. The protein was transferred to nitrocellulose and probed using 1 µg/ml purified anti-L762P rabbit
15 polyclonal sera (lot #690/73) or non-diluted anti-L762P mAb 153.20.1 supernatant. Blots were revealed using either goat anti-rabbit Ig coupled to HRP or goat anti-mouse Ig coupled to HRP followed by incubation in ECL substrate.

For flow cytometric analysis, cells were washed further with ice cold staining buffer (PBS+1%BSA +Azide). Next, the cells were incubated for 30 minutes
20 on ice with 10ug/ml of purified anti-L762P polyclonal sera (lot #690/73) or a 1:2 dilution of anti-L762P mAb 153.20.1 supernatant. The cells were washed 3 times with staining buffer and then incubated with a 1:100 dilution of goat anti-rabbit Ig(H+L)-FITC or goat anti-mouse Ig(H+L)-FITC reagent (Southern Biotechnology) for 30 minutes on ice. After 3 washes, the cells were resuspended in staining buffer containing
25 propidium iodide (PI), a vital stain that allows for the exclusion of permeable cells, and analyzed by flow cytometry.

EXAMPLE 23

GENERATION OF POLYCLONAL ANTIBODIES TO LUNG TUMOR ANTIGENS

Three lung antigens, L523S (SEQ ID NO:176), L763P (SEQ ID NO:159) and L763 peptide #2684 (SEQ ID NO:441), were expressed and purified for use in
5 antibody generation.

L523S and L763P were expressed in an *E. coli* recombinant expression system and grown overnight in LB Broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning, 10 ml of the overnight culture was added to 500 ml of 2x YT with the appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When
10 the optical density of the culture reached 0.4-0.6 at 560 nanometers, the cells were induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were harvested by centrifugation.

The cells were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for
15 future use or immediately processed. Twenty milliliters of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, this mixture was then run through a french press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein.

20 For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8M urea or 6M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-
25 chelate resin (Qiagen) and incubated for 45 minutes to 1 hour at room temperature with continuous agitation.

After incubation, the resin and protein mixture was poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted
30 from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and

collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification.

As a final purification step, a strong anion exchange resin, in this case Hi-Prep Q (Biorad), was equilibrated with the appropriate buffer and the pooled
5 fractions from above were loaded onto the column. Each antigen was eluted off the column with an increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool.

The pooled fractions were dialyzed against 10 mM Tris pH 8.0. The
10 release criteria were purity as determined by SDS-PAGE or HPLC, concentration as determined by Lowry assay or Amino Acid Analysis, identity as determined by amino terminal protein sequence, and endotoxin level was determined by the Limulus (LAL) assay. The proteins were then put in vials after filtration through a 0.22-micron filter and the antigens were frozen until needed for immunization.

15 The L763 peptide #2684 was synthesized and conjugated to KLH and froze until needed for immunization.

The polyclonal antisera were generated using 400 micrograms of each lung antigen combined with 100 micrograms of muramyldipeptide (MDP). An equal volume of Incomplete Freund's Adjuvant (IFA) was added and then mixed and injected
20 subcutaneously (S.C.) into a rabbit. After four weeks, the rabbit was S.C. boosted with 200 micrograms of antigen mixed with an equal volume of IFA. Thereafter the rabbit was I.V. boosted with 100 micrograms of antigen. The animal was bled seven days following each boost. The blood was then incubated at 4°C for 12-24 hours followed by centrifugation to generate the sera.

25 The polyclonal antisera were characterized using 96 well plates coated with antigen and incubated with 50 microliters (typically 1 microgram/microliter) of the polyclonal antisera at 4°C for 20 hours. Basically, 250 microliters of BSA blocking buffer was added to the wells and incubated at room temperature for 2 hours. Plates were washed 6 times with PBS/0.1% Tween. The rabbit sera were diluted in PBS/0.1%
30 Tween/0.1%BSA. 50 microliters of diluted sera was added to each well and incubated

at room temperature for 30 minutes. The plates were washed as described above, and then 50 microliters of goat anti-rabbit horseradish peroxidase (HRP) at a 1:10000 dilution was added and incubated at room temperature for 30 minutes.

The plates were washed as described above, and 100 microliters of TMB
5 Microwell Peroxidase Substrate was added to each well. Following a 15-minute incubation in the dark at room temperature, the colorimetric reaction was stopped with 100 microliters of 1N H₂SO₄ and read immediately at 450 nm. All the polyclonal antibodies showed immunoreactivity to the appropriate antigen. Tables 7-9 show the antibody reactivity of rabbit antisera in serial dilution to the three lung antigens, L523S,
10 L763P and L763 peptide #2684. The first column shows the antibody dilutions. The columns "Pre-immune sera" indicate ELISA data for two experiments using pre-immune sera. These results are averaged in the fourth column. The columns "anti-L523S, L763P or #2684" indicate ELISA data for two experiments using sera from rabbits immunized as described in this Example, using the respective antigen, referred
15 to as either L523S, L763P or #2684 in the tables.

Table 7

Antibody dilution	Pre-immune sera (1)	Pre-immune sera (2)	Average	Anti-L523S (1)	Anti-L523S (2)	Average
1:1000	0.14	0.14	0.14	2.36	2.37	2.37
1:2000	0.12	0.10	0.11	2.29	2.23	2.26
1:4000	0.10	0.09	0.10	2.11	2.17	2.14
1:8000	0.09	0.09	0.09	1.98	2.00	1.99
1:16000	0.09	0.09	0.09	1.73	1.76	1.75
1:32000	0.09	0.09	0.09	1.35	1.40	1.37
1:64000	0.09	0.11	0.10	0.94	0.98	0.96
1:128000	0.09	0.08	0.08	0.61	0.61	0.61
1:256000	0.08	0.08	0.08	0.38	0.38	0.38
1:512000	0.09	0.08	0.08	0.24	0.25	0.25
1:1024000	0.08	0.08	0.08	0.17	0.17	0.17
1:2048000	0.08	0.08	0.08	0.14	0.13	0.13

Table 8

5

Antibody dilution	Pre-immune sera (1)	Pre-immune sera (2)	Average	Anti-L763P (1)	Anti-L763P (2)	Average
1:1000	0.09	0.11	0.10	1.97	1.90	1.93
1:2000	0.07	0.07	0.07	1.86	1.84	1.85
1:4000	0.06	0.06	0.06	1.82	1.81	1.81
1:8000	0.06	0.06	0.06	1.83	1.81	1.82
1:16000	0.06	0.05	0.06	1.79	1.74	1.76
1:32000	0.06	0.06	0.06	1.56	1.51	1.53
1:64000	0.06	0.05	0.05	1.35	1.34	1.35
1:128000	0.05	0.05	0.05	1.01	0.98	0.99
1:256000	0.06	0.05	0.05	0.69	0.70	0.70
1:512000	0.06	0.05	0.05	0.47	0.44	0.46
1:1024000	0.06	0.05	0.06	0.27	0.27	0.27
1:2048000	0.05	0.05	0.05	0.16	0.15	0.16

Table 9

Antibody dilution	Pre-immune sera (1)	Pre-immune sera (2)	Average	Anti-#2684 (1)	Anti-#2684 (2)	Average
1:1000	0.07	0.07	0.07	2.10	2.00	2.05
1:2000	0.07	0.06	0.06	1.95	1.96	1.95
1:4000	0.06	0.06	0.06	1.77	1.82	1.79
1:8000	0.06	0.06	0.06	1.79	1.81	1.80
1:16000	0.06	0.06	0.06	1.54	1.50	1.52
1:32000	0.06	0.06	0.06	1.27	1.20	1.24
1:64000	0.06	0.06	0.06	0.85	0.82	0.83
0	0.06	0.06	0.06	0.06	0.06	0.06

5 Tables 10-12 show the affinity purification of the respective antibodies to the three lung antigens, L523S, L763P and L763 peptide #2684.

Table 10

Antibody conc. (µg/ml)	Affinity pure (salt peak)	Affinity pure (salt peak)	Average	Affinity pure (acid peak)	Affinity pure (acid peak)	Average
1.0	2.38	2.35	2.36	2.25	2.31	2.28
0.5	2.24	2.22	2.23	2.19	2.18	2.18
0.25	2.05	2.09	2.07	2.01	2.03	2.02
0.13	1.70	1.81	1.75	1.74	1.74	1.74
0.063	1.44	1.44	1.44	1.43	1.38	1.40
0.031	1.05	1.05	1.05	0.99	0.99	0.99
0.016	0.68	0.67	0.68	0.65	0.64	0.64
0.0078	0.43	0.42	0.42	0.39	0.39	0.39
0.0039	0.27	0.26	0.27	0.24	0.26	0.25
0.0020	0.18	0.20	0.19	0.19	0.18	0.19
0.0010	0.13	0.14	0.13	0.13	0.14	0.13
0.00	0.11	0.12	0.11	0.10	0.12	0.11

Table 11

Antibody dilution	Affinity pure	Affinity pure	Average
1:1000	1.64	1.77	1.70
1:2000	1.59	1.76	1.68
1:4000	1.48	1.62	1.55
1:8000	1.35	1.43	1.39
1:16000	1.09	1.19	1.14
1:32000	0.81	0.89	0.85
1:64000	0.55	0.58	0.56
1:128000	0.31	0.35	0.33
1:256000	0.18	0.20	0.19
1:512000	0.11	0.12	0.11
1:1024000	0.07	0.07	0.07
1:2048000	0.06	0.06	0.06

Table 12

5

Antibody conc. ($\mu\text{g/ml}$)	Affinity pure	Affinity pure	Average
1.0	2.00	2.02	2.01
0.5	2.01	1.93	1.97
0.25	1.84	1.83	1.84
0.13	1.80	1.83	1.81
0.06	1.39	1.60	1.50
0.03	1.33	1.35	1.34
0.02	0.94	0.93	0.94
0.00	0.06	0.06	0.06

EXAMPLE 24

FULL-LENGTH cDNA SEQUENCE ENCODING L529S

10

The isolation of a partial sequence (SEQ ID NO:106) for lung antigen L529S was previously provided in Example 2. This partial sequence was used as a

query to identify potential full length cDNA and protein sequences by searching against publicly available databases. The predicted full-length cDNA sequence for the isolated cloned sequence of SEQ ID NO:106 is provided in SEQ ID NO:442. The deduced amino acid sequence of the antigen encoded by SEQ ID NO:442 is provided in SEQ ID NO:443. It was previously disclosed in Example 2 that L529S shows similarity to connexin 26, a gap junction protein.

EXAMPLE 25

EXPRESSION IN MEGATERIUM OF A HISTIDINE TAG-FREE L523S FUSION PROTEIN

PCR was performed on the L523S coding region with the following primers:

Forward primer PDM-734 5' caatcaggcatgcacaacaactgtatatcggaac 3'
(SEQ ID NO:444) Tm 63°C.

Reverse primer PDM-735 5' cgtcaagatcttcattacttccgtcttgac 3' (SEQ ID NO:445) TM 60°C.

The PCR conditions were as follows:

10µl 10X Pfu buffer
1.0µl 10mM dNTPs
2.0µl 10µM each primer
83µl sterile water
1.5µl Pfu DNA polymerase (Stratagene, La Jolla, CA)
50ng DNA
96°C for 2 minutes, 96°C for 20 seconds, 62°C for 15 seconds, 72°C for 4 minute with 40 cycles and then 72°C for 4 minutes.

The PCR product was digested with SphI and BglII restriction enzymes, gel purified and then cloned into pMEG-3, which had been digested with SphI and BglII restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into Megaterium cells for expression.

The amino acid sequence of expressed recombinant L523S is shown in SEQ ID NO:446, and the DNA coding region sequence is shown in SEQ ID NO:447.

5

EXAMPLE 26EXPRESSION IN *E. COLI* OF A HISTIDINE TAG-FREE L523S FUSION PROTEIN

PCR was performed on the L552S coding region with the following primers:

10

Forward primer PDM-733 5' cgtactagcatatgaacaaactgtatatcggaac 3' (SEQ ID NO:448) Tm 64°C.

Reverse primer PDM-415 5' ccatagaattcattactccgtcttgactgagg 3' (SEQ ID NO:426) TM 62°C.

The PCR conditions were as follows:

15

10µl 10X Pfu buffer

1.0µl 10mM dNTPs

2.0µl 10µM each primer

83µl sterile water

1.5µl Pfu DNA polymerase (Stratagene, La Jolla, CA)

20

50ng DNA

96°C for 2 minutes, 96°C for 20 seconds, 62°C for 15 seconds, 72°C for 4 minute with 40 cycles and then 72°C for 4 minutes.

The PCR product was digested with NdeI and EcoRI restriction enzymes, gel purified and then cloned into pPDM, a modified pET28 vector, which had been digested with NdeI and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into BLR pLys S and HMS 174 pLys S cells for expression.

25

The amino acid sequence of expressed recombinant L523S is shown in SEQ ID NO:449, and the DNA coding region sequence is shown in SEQ ID NO:450.

30

EXAMPLE 27

EPIOTOPE-ANALYSIS OF L514S AND L523S-SPECIFIC ANTIBODIES

5 Peptides of candidate antigens can be used for the evaluation of antibody responses in both preclinical and clinical studies. These data allow one to further confirm the antibody response against a certain candidate antigen. Protein-based ELISA with and without competitive peptides and peptide-based ELISA can be used to evaluate these antibody responses. Peptide ELISA is especially useful since it can
 10 further exclude the false positive of the antibody titer observed in protein-based ELISA as well as to provide the simplest assay system to test antibody responses to candidate antigens. In this example, data was obtained using both L514S- and L523S-peptides that show that individual cancer patients produce L514S- and L523S-specific antibodies. The L514S-specific antibodies recognize primarily the following epitope of
 15 L514S:

 aa86-110: LGKEVRDAKITPEAFEKLGFPAAKE (SEQ ID NO:451).

 This epitope is the common epitope in humans. A rabbit antibody specific for L514S recognizes two additional epitopes of L514S:

20 (1) aa21-45: KASDGDYYTLAVPMGDVPMGDGISVA (SEQ ID NO:452)

 (2) aa121-135: PDRDVNLTHQLNPKVK (SEQ ID NO:453)

 It was further found that the SEQ ID NO:452 is common to both L514S isoforms, L514S-13160 and L514S-13166, whereas the other epitopes, SEQ ID NO:451
 25 and SEQ ID NO:453, are probably specific to the isoform, L514S-13160.

 The L523S-specific antibodies recognize primarily the following epitope of L523S:

 aa440-460: KIAPAEAPDAKVRMVITGP (SEQ ID NO:454).

 This epitope is the common epitope in humans. A rabbit antibody
 30 specific for L523S recognizes two other epitopes:

(1) aa156-175 PDGAAQQNNNPLQQPRG (SEQ ID
NO:455)

(2) aa326-345: RTITVKGNVETCAKAEEEIM (SED ID
NO:456)

5

In further studies, it was determined by peptide based ELISAs that eight additional epitopes of L523S were recognized by L523S-specific antibodies:

(1) aa40-59 AFVDCPDESWALKAJEALS (SEQ ID
NO:457)

10 (2) aa80-99: IRKLQIRNIPPHLQWEVLDS (SED ID
NO:458)

(3) aa160-179: AQQNPLQQPRGRRGLGQRGS (SEQ ID
NO:459)

15 (4) aa180-199: DVHRKENAGAAEKSITILST (SED ID
NO:460)

(5) aa320-339: LYNPERTITVKGNVETCAKA (SEQ ID
NO:461)

(6) aa340-359: EEEIMKKIRESYENDIASMN (SED ID
NO:462)

20 (7) aa370-389: LNALGLFPPTSGMPPPTSGP (SEQ ID
NO:463)

(8) aa380-399: KIAPAEAPDAKVRMVIITGP (SED ID
NO:464)

25 Out of these, six epitopes are common in both lung plural effusion fluid samples and in sera of lung patients. Of these six, SEQ ID NO:459 and SEQ ID NO:463 have no homology to other L523S-family proteins such as IGF-II mRNA-binding proteins 1 and 2. Accordingly, this indicates that these two peptides can be used as an assay system to determine the antibody response to L523S.

30

EXAMPLE 28

GENERATION OF L523S-SPECIFIC CTL LINES USING IN VITRO WHOLE-GENE PRIMING

To determine if L523S is capable of generating a CD8⁺ T cell immune response, CTLs were generated using *in vitro* whole-gene priming methodologies with tumor antigen-vaccinia infected DC (Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with the L523S tumor antigen, as determined by interferon-gamma ELISPOT analysis. Specifically, dendritic cells (DC) were differentiated from Percoll-purified monocytes derived from PBMC of normal human donors by plastic adherence and growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following the five days of culture, the DC were infected overnight with a recombinant adenovirus that expresses L523S at a multiplicity of infection (M.O.I) of 33, 66 and 100, and matured overnight by the addition of 2 µg/ml CD40 ligand. The virus was then inactivated by UV irradiation. In order to generate a CTL line, autologous PBMC were isolated and CD8⁺ T cells were enriched for by the negative selection using magnetic beads conjugated to CD4⁺, CD14⁺, CD16⁺, CD19⁺, CD34⁺ and CD56⁺ cells. CD8⁺ T cells specific for L523S were established in round bottom 96-well plates using 10,000 L523S expressing DCs and 100,000 CD8⁺ T cells per well in RPMI supplemented with 10% human serum, 10ng/ml of IL-6 and 5ng/ml of IL-12. The cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with L523S, and the costimulatory molecule CD80 in the presence of IL-2. The cells were also stimulated with IFN-gamma to upregulate MHC Class I. The media was supplemented with 10U/ml of IL-2 at the time of stimulation as well as on days 2 and 5 following stimulation. Following three stimulation cycles, ten L523S specific CD8⁺ T cell lines were identified using interferon-gamma ELISPOT analysis that specifically produce interferon-gamma when stimulated with the L523S tumor antigen-transduced autologous fibroblasts, but not with a control antigen.

One line, 6B1, was cloned using anti-CD3 and feeder cells. The clones were tested for specificity on L523S-transduced fibroblasts. In addition, using a panel of HLA-mismatched lines transduced with a vector expressing L523S and measuring interferon-gamma production by this CTL line in an ELISPOT assay, it was determined
5 that this clone 6B1.4B8 is restricted by HLA-A0201.

Also using transfected Cos cells, it was shown that clone 6B1.4B8 recognizes Cos cells transfected with pcDNA3 HLA A0201/L523S in an HLA-restricted and antigen specific manner.

An epitope mapping study demonstrated the clone 6B1.4B8 recognizes
10 HLA-A201 LCL loaded with peptide pool 3 (a polypeptide corresponding to amino acid positions 33-59 of L523S).

A peptide pool breakdown study demonstrated that clone 6B1.4B8 recognizes autologous B-LCL loaded with 15-mer peptides from amino acid positions 37-55 of L523S, TGYAFVCPDESWALKAE (SEQ ID NO:465). A further peptide
15 breakdown study demonstrated that clone 6B1.4B8 recognizes T2 cells loaded with the same 15-mer peptides.

A peptide recognition study demonstrated that clone 6B1.4B8 prefers T2 cells loaded with the peptide FVDCPESWAL (SEQ ID NO:466) which corresponds to the amino acid sequence at positions 41-51 of L523S and is encoded by the DNA
20 sequence of SEQ ID NO:467.

EXAMPLE 29

L523S EXPRESSION IN OTHER HUMAN CANCERS

25 It was previously disclosed in Example 2 that L523S is expressed in lung cancers including squamous, adenocarcinoma and small cell carcinoma. EST profiling analysis of L523S further indicates that this protein may also be expressed in a number of other tumor types, including colon adenocarcinomas, prostate adenocarcinomas, CML, AML, Burkitt's Lymphoma, brain tumors, retinoblastomas, ovarian tumors,

teratocarcinomas, uterus myosarcomas, germ cell tumors as well as pancreatic and cervical tumor cell lines.

From the foregoing it will be appreciated that, although specific
5 embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:

- (a) sequences provided in SEQ ID NOs:351, 353, 358, 362, 364, 366, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467;
- (b) complements of the sequences provided in SEQ ID NOs:351, 353, 358, 362, 364, 366, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467;
- (c) sequences consisting of at least 10 contiguous residues of a sequence provided in SEQ ID NOs:351, 353, 358, 362, 364, 366, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467;
- (d) sequences that hybridize to a sequence provided in SEQ ID NOs:351, 353, 358, 362, 364, 366, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467, under highly stringent conditions;
- (e) sequences having at least 75% identity to a sequence of SEQ ID NOs:351, 353, 358, 362, 364, 366, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467;
- (f) sequences having at least 90% identity to a sequence of SEQ ID NOs:351, 353, 358, 362, 364, 366, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467; and
- (g) degenerate variants of a sequence provided in SEQ ID NOs:351, 353, 358, 362, 364, 366, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467.

2. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- (a) sequences having at least 90% identity to a polypeptide having an amino acid sequence of any one of the sequences provided in SEQ ID NOs:352, 354, 357, 361, 363, 365, 367, 369, 376-382, 387-419, 423, 427, 430, 433, 441, 443, 446, 449 and 451-466;

- (b) sequences encoded by a polynucleotide of claim 1;
- (c) sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 1; and
- (d) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 1.

3. An expression vector comprising a polynucleotide of claim 1 operably linked to an expression control sequence.

4. A host cell transformed or transfected with an expression vector according to claim 3.

5. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 2.

6. A method for detecting the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 2;
- (c) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

7. A fusion protein comprising at least one polypeptide according to claim 2.

8. A fusion protein according to claim 9, wherein the fusion protein is selected from the group consisting sequences provided in SEQ ID NOs:352, 354, 423, 427, 430 and 433.

9. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NOs:351, 353, 358, 362, 364, 366, 368, 370-375, 420, 424, 428, 431, 434, 442, 447, 450 and 467 under highly stringent conditions.

10. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

- (a) polypeptides according to claim 2;
- (b) polynucleotides according to claim 1; and
- (c) antigen-presenting cells that express a polynucleotide according to claim 1,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

11. An isolated T cell population, comprising T cells prepared according to the method of claim 10.

12. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 2;
- (b) polynucleotides according to claim 1;
- (c) antibodies according to claim 5;
- (d) fusion proteins according to claim 7;
- (e) T cell populations according to claim 11; and

(f) antigen presenting cells that express a polypeptide according to claim 2.

13. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 12.

14. A method for the treatment of a lung cancer in a patient, comprising administering to the patient a composition of claim 12.

15. A method for determining the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide according to claim 9;
- (c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and
- (d) compare the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

16. A diagnostic kit comprising at least one oligonucleotide according to claim 9.

17. A diagnostic kit comprising at least one antibody according to claim 5 and a detection reagent, wherein the detection reagent comprises a reporter group.

18. A method for the treatment of lung cancer in a patient, comprising the steps of:

(a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of: (i) polypeptides according to claim 2; (ii) polynucleotides according to claim 1; and (iii) antigen presenting cells that express a polypeptide of claim 2, such that T cell proliferate;

(b) administering to the patient an effective amount of the proliferated T cells,

and thereby inhibiting the development of a cancer in the patient.

SEQUENCE LISTING

<110> Corixa Corporation
 Wang, Tongtong
 Marnerakis, Margarita
 Fanger, Gary R.
 Vedvick, Thomas S.
 Carter, Darrick
 Watanabe, Yoshihiro
 Henderson, Robert A.
 Peckham, David W.
 Fanger, Neil

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 AND DIAGNOSIS OF LUNG CANCER

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gtactagcta caaattcggg ttcatattct acttaacaat ttaaataaac tgaaatattt 540
ctagatggtc tacttctgtt catataaaaa caaaacttga tttccaaaaa aaaaaaaaaa 600
aa 602
```

<210> 12

<211> 685

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 170, 279, 318, 321, 322, 422, 450, 453, 459, 467, 468, 470, 473, 475, 482, 485, 486, 491, 498, 503, 506, 509, 522, 526, 527, 528, 538, 542, 544, 551, 567, 568, 569, 574, 576, 582, 587, 588, 589, 590, 592, 593, 598, 599, 603, 605, 608

<223> n = A,T,C or G

<221> misc_feature

<222> 633, 634, 635, 644, 646, 648, 651, 655, 660, 662, 663, 672, 674, 675, 682, 683

<223> n = A,T,C or G

<400> 12

```
actagtcctg tgaaagtaca actgaaggca gaaagtgtta ggattttgca tctaattgttc 60
attatcatgg tattgatgga cctaagaaaa taaaaattag actaagcccc caaataagct 120
gcatgcattt gtaacatgat tagtagattt gaatatatag atgtagtatn ttgggtatct 180
agggttttta tcattatgta aaggaattaa agtaaaggac tttgtagtgt tttttattaa 240
atatgcatat agtagagtgc aaaaatatag caaaaatana aactaaaggt agaaaagcat 300
```

```

ttagatatg ccttaatnta nnaactgtgc caggtggccc tcggaataga tgccaggcag 360
agaccagtgc ctgggtggtg cctccccttg tctgcccccc tgaagaactt cctcacgtg 420
angtagtgcc ctcgtaggtg tcacgtggan tantggganc aggccgnncn gtnanaagaa 480
ancanngtga nagtttcncc gtngangcng aactgtccct gngccnnnac gctcccanaa 540
cntntccaat ngacaatcga gtttccnnnc tccngnaacc tngccgnnnn cnggcccnnc 600
cantntgnta accccgcgcc cggatcgctc tcnnntcgtt ctncncnaa ngggnnttcn 660
cnnccgcgct cncnnccccg cnncc

```

685

<210> 13

<211> 694

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 503, 546, 599, 611, 636, 641, 643, 645, 656, 658, 662, 676, 679, 687

<223> n = A,T,C or G

<400> 13

```

cactagtcac tcattagcgt tttcaatagg gctcttaagt ccagtagatt acgggtagtc 60
agttgacgaa gatctgggtt acaagaacta attaatgtt tcattgcatt tttgtaagaa 120
cagaataatt ttataaaatg tttgtagttt ataattgccg aaaataattt aaagacactt 180
tttctctgtg tgtgcaaatg tgtgtttgtg atccattttt tttttttttt taggacacct 240
gtttactagc tagcttttaca atatgccaaa aaaggatttc tccctgacct catccgtggt 300
tcaccctctt ttccccccat gctttttgcc ctagtattata acaaaggaat gatgatgatt 360
taaaaagtag ttctgtatct tcagtatctt ggtcttccag aacctcttgg ttgggaaggg 420
gatcattttt tactggatcat ttcccttttg agtgactac ttttaacagat ggaaagaact 480
cattggccat ggaaacagcc gangtggtg gagccagcag tgcattggac cgtccggcat 540
ctggcgtgat tggctctggct gccgtcattg tcagcacagt gccatgggac atggggaana 600
ctgactgcac ngccaatggt tttcatgaag aatacngcat ncnngtgat cacgtnancc 660
angacgctat gggggncana gggccanttg ctcc

```

694

<210> 14

<211> 679

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 29, 68, 83, 87, 94, 104, 117, 142, 145, 151, 187, 201, 211, 226, 229, 239, 241, 245, 252, 255, 259, 303, 309, 359, 387, 400, 441, 446, 461, 492, 504, 505, 512, 525, 527, 533, 574, 592, 609, 610, 618, 620, 626, 627, 633, 639, 645, 654

<223> n = A,T,C or G

<400> 14

```

cagccgcctg catctgtatc cagcgccang tcccgccagt cccagctgcg cgcgcccccc 60
agtcccgncac ccgttcggcc cangctnagt tagnctcac catnccggtc aaaggangca 120
ccaagtgcac caaatccctg cngtncggat ntaaatccat cttctggctt gccgggattg 180
ctgtccntgc cattggacta nggctccgat ncgactotca gaccanganc atcttcganc 240
naganactaa tnatnatntt tccagcttct acacaggagt ctatattctg atcggtatccg 300
gcnccctcnt gatgctggtg ggcttcctga gctgctgcgg ggctgtgcaa gactcccant 360
gcatgctggg actgttcttc ggcttcntct tggatgatn cgccattgaa atacctgcgg 420
ccatctgggg atattccact ncgatnatgt gattaaggaa ntccacggag ttttacaagg 480
acacgtacaa cnacctgaaa accnnggatg anccccaccg ggaancnctg aangccatcc 540
actatgcgtt gaactgcaat ggtttggctg gggnccctga acaatttaac cncatacatc 600
tggcccccann aaaggacntn ctcgannccct tcnccgtgna attcngttct gatnccatca 660

```

cagaagtctc gaacaatcc

679

<210> 15

<211> 695

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 105, 172, 176, 179, 189, 203, 212, 219, 221, 229, 231, 238,
242, 261, 266, 270, 278, 285, 286, 298, 311, 324, 337, 350,
363, 384, 391, 395, 405, 411, 424, 427, 443, 448, 453, 455,
458, 463, 467, 470, 479, 482, 484, 493, 499, 505, 518

<223> n = A,T,C or G

<221> misc_feature

<222> 520, 523, 531, 540, 584, 595, 597, 609, 611, 626, 628, 651,
652, 657, 661, 665, 669, 672, 681, 683, 691, 693

<223> n = A,T,C or G

<400> 15

```
actagtggat aaaggccagg gatgctgctc aacctcctac catgtacagg gacgtctccc 60
cattacaact acccaatccg aagtgtcaac tgtgtcagga ctaanaaacc ctggttttga 120
ttaaaaaagg gcctgaaaaa aggggagcca caaatctgtc tgcttcctca cnttantcnt 180
tggcaaatna gcattctgtc tcnttggtg cngcctcanc ncaaaaaanc ngaactcnat 240
cnggccagg aatacatctc ncaatnaacn aaattganca aggcnnntggg aaatgccnga 300
tgaggattatc ntccgcttgt tganccttcta agtttcnttc ccttcattcn accctgccag 360
ccnagttctg ttagaaaaat gccngaattc naacnccggt tttcntactc ngaattttaga 420
tctncanaaa ctctcctggcc acnattcnaa tt nanggnca cgnacanatn ccttccatna 480
ancncacccc acntttgana gccangacaa tgactgcntn aantgaaggc ntgaaggaan 540
aactttgaaa ggaaaaaaa ctttgtttcc ggccccttcc aacncttctg tgttnancac 600
tgccctctng naaccctgga agcccnngna cagtgttaca tgttgttcta nnaaacngac 660
ncttnaatnt cnatcttccc nanaacgatt ncnc 695
```

<210> 16

<211> 669

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 299, 354, 483, 555, 571, 573, 577, 642, 651, 662, 667

<223> n = A,T,C or G

<400> 16

```
cgccgaagca gcagcgcagg ttgtccccgt tccccctccc ccttcccttc tccggttgcc 60
ttccccggcc ccttacactc cacagtcccg gtcccgccat gtcccagaaa caagaagaag 120
agaaccctgc ggaggagacc ggcgaggaga agcaggacac gcaggagaaa gaaggtattc 180
tgccctgagag agctgaagag gcaaagctaa aggccaaata cccaagccta ggacaaaagc 240
ctggaggctc cgacttcctc atgaagagac tccagaaagg gcaaaagtac tttgactcng 300
gagactacaa catggccaaa gccaacatga agaataagca gctgccaagt gcangaccag 360
acaagaacct ggtgactggg gatcacatcc ccacccaca ggatctgccc agagaaagtc 420
ctcgtctgtc accagcaagc ttgcgggtgg ccaagttgaa tgatgctgcc ggggctctgc 480
canatctgag acgcttcctt ccctgcccc cccgggtcct gtgctggctc ctgcccttcc 540
tgcttttgca gccannggtc aggaagtggc ncnggtngtg gctggaaagc aaaacccttt 600
cctgttggtg tcccacccat ggagcccctg gggcgagccc angaacttga ncctttttgt 660
tntcttncc 669
```

<210> 17
<211> 697
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 33, 48, 50, 55, 59, 60, 76, 77, 78, 90, 113, 118, 130, 135,
141, 143, 150, 156, 166, 167, 170, 172, 180, 181, 190, 192,
194, 199, 201, 209, 212, 224, 225, 226, 230, 233, 234, 236,
242, 244, 251, 253, 256, 268, 297, 305, 308, 311, 314
<223> n = A,T,C or G

<221> misc_feature
<222> 315, 317, 322, 324, 327, 333, 337, 343, 362, 364, 367, 368,
373, 384, 388, 394, 406, 411, 413, 423, 429, 438, 449, 450,
473, 476, 479, 489, 491, 494, 499, 505, 507, 508, 522, 523,
527, 530, 533, 535, 538, 539, 545, 548, 550, 552, 555
<223> n = A,T,C or G

<221> misc_feature
<222> 562, 563, 566, 568, 572, 577, 578, 580, 581, 591, 594, 622,
628, 632, 638, 642, 644, 653, 658, 662, 663, 665, 669, 675,
680, 686, 689
<223> n = A,T,C or G

<400> 17
gcaagatatg gacaactaag tgagaaggta atnctctact gctctagntn ctcnnggcnn 60
gacgcgctga ggagannnac gctggcccan ctgccggcca cacacgggga tontggtnat 120
gcctgcccان gggancccca ncctcggan ccatntcac acccgnnccn tncgcccacn 180
ncctggetcn cncngcccng nccagctcnc gnccccctcc gccnnnctcn ttncntctc 240
cncnccctcc ncnacnacct cctaccncng gctccctccc cagccccccc ccgcaancct 300
ccacnacncc ntccnncnca anccnccnctc gcnctcngcc ccngccccct gcccccgcgc 360
cncnacnncg cgnccccccg cgcncgcngc ctccccccct cccacnacag ncnacccgcg 420
agncaagcnc tccgcccncct gacgcccenn cccgcgcgcg tcaccttcat ggncnncng 480
ccccgctcnc nccnctgcnc gccgncnngg cgcgccgccc cncnccngtn ccnccgngg 540
ccccngcngn angcngtgcg cnnccangncc gngccgnncn ncacctccg nccnccgccc 600
cgcccgcgtgg gggctcccgc cncgcggntc antccccncc cntncgcca ctntccgntc 660
cnnnctcnc gctcngcgcn cgccnccnc cccccc 697

<210> 18
<211> 670
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 234, 292, 329, 437, 458, 478, 487, 524, 542, 549, 550, 557,
576, 597, 603, 604, 646, 665
<223> n = A,T,C or G

<400> 18
ctcgtgtgaa ggggtgcagta cctaagccgg agcggggtag aggcggggccg gcacccccctt 60
ctgacctcca gtgcgcgcgg cctcaagatc agacatggcc cagaacttga acgacttggc 120
gggacggctg cccgcccggc cccggggcat gggcacggcc ctgaagctgt tgctgggggc 180
cggcgccgtg gcctacggtg tgcgcgaatc tgtgttcacc gtggaaggcg ggcnacagagc 240
catcttcttc aatcggtatc gtggagtga caggacacta tcttggggcg anggccttca 300
cttcaggatc cttggttcca gtacccanc atctatgaca ttcggggccag acctcgaaaa 360

```

aatctcctcc ctacaggctc caaagaccta cagatgggtga atatctccct gcgagtgttg 420
tctcgaccaa tgctcangaa cttcctaaca tgttccancg cctaagggct ggactacnaa 480
gaacgantgt tgccgtccat tgtcacgaag tgctcaagaa ttnggtggc caagttcaat 540
gncctcacnn ctgatcnccc agcggggcca agttanccct ggttgatccc cgggganctg 600
acnnaaaagg gccaaaggact tcöcctcatc ctggataatg tggcncac aaagctcaac 660
tttanccacc                                     670

```

```

<210> 19
<211> 606
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 506
<223> n = A,T,C or G

```

```

<400> 19
actagtgcc aactcagctc ccaggccagt tctctgaatg tgcaggagt ccaggatctc 60
tggcctcagt tgctccttgg tattgatggg ggacaaattg gggatggcca gagccccgag 120
tgtcgccctg gctcaactgt ggttgatttg tctgtgccc gaaagtttg catcattcgt 180
ccaggctgtg ccctggaaag tactacagcc atcctccaac agaagtacgg actgctcccc 240
tcacatgcgt cctacctgtg aaactctggg aagcaggaag gcccaagacc tgggtgctgga 300
tactatgtgt ctgtccactg acgactgtca aggcctcatt tgcagaggcc accggagcta 360
gggcactagc ctgactttta aggcatgtgt tctttctgag cactgtagac caagcccttg 420
gagctgctgg tttagccttg cacctgggga aaggatgtat ttatttgtat tttcatatat 480
cagccaaaag ctgaatggaa aagttnagaa cattcctagg tggccttatt ctaataagtt 540
tcttctgtct gttttgtttt tcaattgaaa agttattaaa taacagattt agaatctagt 600
gagacc                                     606

```

```

<210> 20
<211> 449
<212> DNA
<213> Homo sapiens

```

```

<400> 20
actagtaaac aacagcagca gaaacatcag tatcagcagc gtcgccagca ggagaatatg 60
cagcgccaga gccgaggaga acccccgctc cctgaggagg acctgtccaa actcttcaaa 120
ccaccacagc cgccgtgccg gatggactcg ctgctcattg caggccagat aaacacttac 180
tgccagaaca tcaaggagt cactgccc aaacttaggca agctcttcat ggcccaggct 240
cttcaagaat acaacaacta agaaaaggaa gtttccagaa aagaagttaa catgaactct 300
tgaagtcaca ccagggaac tcttggaa aatatatttg catattgaaa agcacagagg 360
atctctttag tgctcattgcc gattttggct ataacagtgt ctttctagcc ataataaaat 420
aaaacaaaat cttgactgct tgctcaaaa                                     449

```

```

<210> 21
<211> 409
<212> DNA
<213> Homo sapiens

```

```

<400> 21
tatcaatcaa ctggtgaata attaaacaat gtgtggtgtg atcatacaaa gggtagcact 60
caatgataaa aggaacaagc tgcctatatg tggaacaaca tggatgcatt tcagaaactt 120
tatgttgagt gaaagaacaa acacggagaa cactactatg ggttctcttt atgtaacatt 180
acagaaataa aaacagaggc aaccaccttt gaggcagtat ggagtgagat agactggaaa 240
aagggaaggaa ggaaactcta cgctgatgga aatgtctgtg tcttcattgg gtggtagtta 300
tgtggggata tacatttgtc aaaatttatt gaactatata ctaaagaact ctgcatttta 360
ttgggatgta aataatacct caattaaaaa gacaaaaaaa aaaaaaaaaa 409

```

<210> 22
<211> 649
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 263, 353, 610, 635, 646
<223> n = A,T,C or G

<400> 22
acaattttca ttatcttaag cacattgtac atttctacag aacctgtgat tattctcgca 60
tgataaggat ggtacttgca tatggtgaat tactactgtt gacagtttcc gcagaaatcc 120
tatttcagtg gaccaacatt gtggcatggc agcaaatgcc aacattttgt ggaatagcag 180
caaatctaca agagaccctg gttgggtttt cgttttggtt tctttgtttt tcccccttc 240
tcctgaatca gcagggatgg aangagggtg gggaagtatt gaattactcc ttccagtagt 300
agctctgaag tgtcacattt aatatcagtt ttttttaaac atgattctag ttnaatgtag 360
aagagagaag aaagaggaag tgttcacttt ttttaatacac tgatttagaa atttgatgtc 420
ttatatcagt agttctgagg tattgatagc ttgctttatt tctgccttta cgttgacagt 480
gttgaagcag ggtgaataac taggggcata tatatttttt ttttttgtaa gctgtttcat 540
gatgttttct ttggaatttc cggataagtt caggaaaaca tctgcatgtt gttatctagt 600
ctgaagttn tatccatctc attacaacaa aaacnccag aacggnntg 649

<210> 23
<211> 669
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 642, 661
<223> n = A,T,C or G

<400> 23
actagtgccg tactggctga aatccctgca ggaccaggaa gagaaccagt tcagactttg 60
tactctcagt caccagctct ggaattagat aaattccttg aagatgtcag gaatgggac 120
tatcctctga cagcctttgg gctgcctcgg cccagcagc cacagcagga ggaggtgaca 180
tcacctgtcg tgccccctc tgtcaagact ccgacacctg aaccagctga ggtggagact 240
cgcaaggtgg tgctgatgca gtgcaacatt gagtcggtgg aggaggaggt caaacaccac 300
ctgacacttc tgctgaagtt ggaggacaaa ctgaaccggc acctgagctg tgacctgatg 360
ccaaatgaga atatccccga gttggcggct gagctggtgc agctgggctt cattagttag 420
gctgaccaga gccggttgac ttctctgcta gaagagactt gaacaagttc aattttgcca 480
ggaacagtac cctcaactca gccgctgtca ccgtctcctc ttagagctca ctggggccag 540
gccctgatct gcgctgtggc tgtcctggac gtgctgcacc ctctgtcctt cccccagtc 600
agtattacct gtgaagccct tccctccttt attattcagg anggctgggg gggctccttg 660
nttctaacc 669

<210> 24
<211> 442
<212> DNA
<213> Homo sapiens

<400> 24
actagtacca tcttgacaga ggatacatgc tccccaaaacg tttgttacca cacttaaaaa 60
tcaactgcat cattaagcat cagtttcaaa attatagcca ttcattgattt actttttcca 120
gatgactatc attattctag tcctttgaat ttgtaagggg aaaaaaaaca aaaacaaaaa 180
cttacgatgc actttttctc agcacatcag atttcaaatt gaaaattaaa gacatgctat 240

```

ggtaatgcac ttgctagtag tacacacttt ggtacaacaa aaaacagagg caagaaacaa 300
cggaagaga aaagccttcc ttgttggcc cttaactga gtcaagatct gaaatgtaga 360
gatgatctct gacgatacct gtatgttctt attgtgtaaa taaaattgct ggtatgaaat 420
gacctaaaaa aaaaaaaga aa 442

```

```

<210> 25
<211> 656
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 330, 342, 418, 548, 579, 608
<223> n = A,T,C or G

```

```

<400> 25
tgcaagtacc acacactggt tgaattttgc acaaaaagt actgtaggat caggtagatag 60
ccccggaatg tacagtgtct tggcgacca agatgccttc taaaggctga cataccttgg 120
accctaattg ggcagagagt atagccctag cccagtgggt acatgaccac tccctttggg 180
aggcctgagg tagaggggag tggtagtgt tttctcagt gaagcagcac atgagtgggt 240
gacaggatgt tagataaagg ctctagttag ggtgtcattg tcatttgaga gactgacaca 300
ctcctagcag ctggtaaagg ggtgctggan gccatggagg anctctagaa acattagcat 360
gggctgactc gattacttcc tggcatcccg ctcactttta tgggaagtct tattagangg 420
atgggacagt ttccatatac cttgctgtgg agctctgga cactctctaa atttccctct 480
atataaaatc actgccctaa ctacacttcc tccttgaagg aatagaaatg gaactttctc 540
tgacatannt cttggcatgg ggagccagcc acaaatgana atctgaacgt gtccagggtt 600
ctcctganac tcactctacat agaattggtt aaaccctccc ttggaataag gaaaaa 656

```

```

<210> 26
<211> 434
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 395
<223> n = A,T,C or G

```

```

<400> 26
actagttcag actgccacgc caaccccaga aaatacccca catgccagaa aagtgaagtc 60
ctagggtgtt ccatctatgt ttcaatctgt ccatctacca ggcctcgaga taaaaacaaa 120
acaaaaaac gctgccaggt tttagaagca gttctggtct caaaaccatc aggatcctgc 180
caccagggtt cttttgaaat agtaccacat gtaaaaggga atttggcttt cacttcatct 240
aataactgaa ttgtcaggct ttgattgata attgtagaaa taagtagcct tctgttggtg 300
gaataagtta taatcagtat tcactctctt gttttttgtc actcttttct ctctaattgt 360
gtcatttgta ctgtttgaaa aatatttctt ctatnaaatt aaactaacct gccttaaaaa 420
aaaaaaaaaa aaaa 434

```

```

<210> 27
<211> 654
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 505, 533, 563, 592, 613, 635, 638
<223> n = A,T,C or G

```

<400> 27

```
actagtccaa cacagtcaga aacattgttt tgaatcctct gtaaaccaag gcattaatct 60
taataaaacca ggatccattt aggtaccact tgatataaaa aggatatcca taatgaatat 120
tttatactgc atccttttaca ttagccacta aatacgttat tgcttgatga agacctttca 180
cagaatccta tggattgcag catttcactt ggctacttca taccatgcc ttaaagaggg 240
gcagtttctc aaaagcagaa acatgccgcc agttctcaag ttttcctcct aactccattt 300
gaatgtaagg gcagctggcc cccaatgtgg ggaggtccga acattttctg aattcccatt 360
ttcttgttcg cggctaaatg acagtttctg tcattactta gattccgatac tttcccaaag 420
gtgttgattt acaaagaggc cagctaatac cagaaatcat gaccctgaaa gagagatgaa 480
attcaagctg ttgagccaggc agganctcag tatggcaaag gtcttgagaa tcngccattt 540
ggtacaaaaa aaatttttaa gcntttatgt tataccatgg aaccatagaa anggcaaggg 600
aattgttaag aanaatttta agtgtccaga cccanaanga aaaaaaaaaa aaaa 654
```

<210> 28

<211> 670

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 101, 226, 274, 330, 385, 392, 397, 402, 452, 473, 476, 532,
534, 538, 550, 583, 595, 604, 613, 622, 643, 669

<223> n = A,T,C or G

<400> 28

```
cgtgtgcaca tactgggagg atttccacag ctgcacggtc acagccctta cggattgcc 60
ggaaggggcg aaagatatgt gggataaact gagaaaagaa nccaaaaacc tcaacatcca 120
aggcagctta ttcgaactct gcggcagcgg caacggggcg gcgggggtccc tgctcccgcc 180
gttcccggtg ctctctcggc agcttttagcg acctgncttt ccttctgagc 240
gtggggccag cccccccgc ggcgccacc cacnctcact ccatgctccc ggaaatcgag 300
aggaagatca ttagttcttt ggggacgttn gtgattctct gtgatgctga aaaacactca 360
tatagggaat gtgggaaatc ctganctctt tnttatntcg tntgatttct tgtgttttat 420
ttgccaaaat gttaccaatc agtgaccaac cnagcacagc caaaaatcgg acntcngctt 480
tagtccgtct tcacacacag aataagaaaa cggcaaaccc accccacttt tnantttnat 540
tattactaan ttttttctgt tgggcaaaag aatctcagga acngccctgg ggccnccgta 600
ctanagttaa ccnagctagt tncatgaaaa atgatgggct ccnctcaat gggaaagcca 660
agaaaaagnc 670
```

<210> 29

<211> 551

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 336, 474, 504, 511, 522, 523, 524, 540, 547

<223> n = A,T,C or G

<400> 29

```
actagtcctc cacagcctgt gaatccccct agacctttca agcatagtga gcggagaaga 60
agatctcagc gtttagccac cttaccocat cctgatgatt ctgtagaaaa ggtttcttct 120
ccctctccag ccactgatgg gaaagtattc tccatcagtt ctcaaaatca gcaagaatct 180
tcagtaccag aggtgcctga tgttgacat ttgccacttg agaagctggg accctgtctc 240
cctcttgact taagtcgtgg ttcagaagtt acagcaccgg tagcctcaga ttctctttac 300
cgtaatgaat gtcccagggc agaaaaagag gatacnaga tgcttccaaa tccttcttcc 360
aaagcaatag ctgatgggaa gaggagctcc agcagcagca ggaatatcga aaacagaaaa 420
aaaagtgaat ttgggaagac aaaagctcaa cagcatttgg taaggagaaa aganaagatg 480
aggaaggaag agagaagaga gacnaagatc nctacggacc gnnncggaag aagaagaagn 540
```


aaaaaanaaa a

551

<210> 30

<211> 684

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 545, 570, 606, 657, 684

<223> n = A,T,C or G

<400> 30

```

actagttcta tctggaaaaa gcccggttg gaagaagctg tggagagtgc gtgtgcaatg 60
cgagactcat ttcttggaag catccctggc aaaaatgcag ctgagtacaa ggttatcact 120
gtgatagaac ctggactgct ttttgagata atagagatgc tgcagtctga agagacttcc 180
agcacctctc agttgaaatga attaatgatg gcttctgagt caactttact ggctcaggaa 240
ccacgagaga tgactgcaga tgtaatcgag cttaaaggga aattcctcat caacttagaa 300
ggtggtgata ttctggaaga gtcttcctat aaagtaattg tcatgccgac tacgaaagaa 360
aaatgcccc gttgttgga gtatacagcg ggagtcctca gatacactgt gtcctcgatg 420
tgcagaagtt gtcagtggga aaatagtatt aacagctcac tcgagcaaga accctcctga 480
cagtactggg ctgaagttt ggatggatta ttacaatat aggaaagaaa gccaagaatt 540
aggtnatgag tggatgagta aatggtggan gatggggaat tcaaatacaga attatggaag 600
aagtnttcc tgttactata gaaaggaatt atgtttattt acatgcagaa aatatanatg 660
tgtggtgtgt accgtggatg gaan                                     684

```

<210> 31

<211> 654

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 326, 582, 651

<223> n = A,T,C or G

<400> 31

```

gcgcagaaaa ggaaccaata tttcagaaac aagcttaata ggaacagctg cctgtacatc 60
aacatcttct cagaatgacc cagaagttat catcgtggga gctggcgtgc ttggctctgc 120
tttggcagct gtgctttcca gagatggaag aaaggtgaca gtcattgaga gagacttaaa 180
agagcctgac agaatagttg gagaattcct gcagccgggt ggttatcatg ttctcaaaga 240
ccttgggtctt ggagatacag tggaaggtct tgatgccag gttgtaaatg gttacatgat 300
tcatgatcag ggaaagcaaa tcagangttc agattcctta ccctctgtca gaaaacaatc 360
aagtgcagag tggaaagagct ttccatcacg gaagattcat catgagtctc cggaagcag 420
ctatggcaga gcccaatgca aagtttattg aaggtgttgt gttacagtta ttagaggaaag 480
atgatgttgt gatgggagtt cagtacaagg ataaagagac tgggagatat caaggaaactc 540
catgctccac tgactgttgt tgcagatggg cttttctcca anttcaggaa aagcctggtc 600
tcaataaagt ttctgtatca ctcatattgt tggcttctta tgaagaatgc nccc 654

```

<210> 32

<211> 673

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 376, 545, 627

<223> n = A,T,C or G

<400> 32

```

actagtgaag aaaaagaaat tctgatacgg gacaaaaatg ctcttcaaaa catcattctt 60
tatcacctga caccaggagt ttctattgga aaaggatttg aacctggtgt tactaacatt 120
ttaaagacca cacaaggaag caaaatcttt ctgaaagaag taaatgatac acttctggtg 180
aatgaattga aatcaaaaga atctgacatc atgacaacaa atggtgtaat tcatgttgta 240
gataaactcc tctatccagc agacacacct gttggaaatg atcaactgct ggaaatactt 300
aataaattaa tcaaatacat ccaaattaag tttgttcgtg gtagcacctt caaagaaatc 360
cccgtgactg tctatnagcc aattattaaa aaatacacca aaatcattga tgggagtgcc 420
tgtgggaaat aactgaaaaa gagaccgaga agaacgaatc attacagggtc ctgaaataaa 480
atacctagga tttctactgg aggtggagaa acagaagaac tctgaagaaa ttgttacaag 540
aagangtccc aagggtacca aattcattga aggtggtgat ggtctttatt tgaagatgaa 600
gaaattaaaa gacgcttcag ggagacnccc catgaaggaa ttgccagcca caaaaaaatt 660
cagggattag aaa

```

673

<210> 33

<211> 673

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 325, 419, 452, 532, 538, 542, 571, 600, 616, 651, 653, 672

<223> n = A,T,C or G

<400> 33

```

actagttatt tactttctc cgcttcagaa ggtttttcag actgagagcc taagcatact 60
ggatctgttg tttcttttgg gtctcacctc atcagtgtgc atagtggcag aaattataaa 120
gaaggttgaa aggagcaggg aaaagatcca gaagcatggt agttcgacat catcatcttt 180
tcttgaagta tgatgcatat tgcattattt tatttgcaaa ctaggaattg cagtctgagg 240
atcatttaga agggcaagtt caagaggata tgaagatttg agaacttttt aactattcat 300
tgactaaaaa tgaacattaa tgttnaagac ttaagacttt aacctgctgg cagtccaaa 360
tgaaattatg caactttgat atcatattcc ttgatttaaa ttgggctttt gtgattgant 420
gaaactttat aaagcatatg gtcagttatt tnattaaaaa ggcaaacct gaaccacctt 480
ctgcacttaa agaagtctaa cagtacaaat acctatctat cttagatgga tntatttntt 540
tntattttta aatattgtac tatttatggt nggtggggct ttcttactaa tacacaaatn 600
aatttatcat ttcaanggca ttctatttgg gtttagaagt tgattccaag nantgcatat 660
ttcgctactg tnt

```

673

<210> 34

<211> 684

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 414, 472, 480, 490, 503, 507, 508, 513, 523, 574, 575, 598, 659, 662, 675

<223> n = A,T,C or G

<400> 34

```

actagtttat tcaagaaaag aacttactga ttcctctgtt cctaaagcaa gagtggcagg 60
tgatcagggc tgggtgtagca tccggttcct ttagtgacgc taactgcatt tgtcactgat 120
gaccaaggag gaaatcacta agacatttga gaagcagtg tatgaacgtt cttggacaag 180
ccacagttct gagccttaac cctgtagttt gcacacaaga acgagctcca cctccccttc 240
ttcaggagga atctgtgcgg atagattggc tggacttttc aatggttctg ggttgcaagt 300
gggcactgtt atggctgggt atggagcggg cagcccagg aatcagagcc tcagcccggc 360
tgcctgggtt gaaggtacag gtgttcagca ccttcggaaa aagggcataa agtngtgggg 420

```

```

gacaattctc agtccaagaa gaatgcattg accattgctg gctatttgct tncctagtan 480
gaattggatn catTTTTgac cangatnntt ctncatgct ttnttgcaat gaaatcaaat 540
cccgcattat ctacaagtgg tatgaagtcc tgcnnccccc agagaggctg ttcaggcnat 600
gtcttccaag ggcagggtgg gttacaccat ttacctccc ctctccccc agattatgna 660
cncagaagga atttntttcc tccc                                     684

```

<210> 35
 <211> 614
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 17, 20, 152, 223, 267, 287, 304, 306, 316, 319, 321, 355,
 365, 382, 391, 407, 419, 428, 434, 464, 467, 477, 480, 495,
 499, 505, 515, 516, 522, 524, 527, 542, 547, 549, 567, 572,
 576, 578
 <223> n = A,T,C or G

```

<400> 35
actagtccaa cgcgttngcn aatattcccc tggtagccta ctcccttacc cccgaatatt 60
ggtaagatcg agcaatggct tcaggacatg ggttctcttc tcctgtgatc attcaagtgc 120
tcaactgatg aagactggct tgtctcagtg tntcaacctc accagggctg tctcttggtc 180
cacacctcgc tccctgttag tgccgtatga cagcccccac canatgacct tggccaagtc 240
acggtttctc tgtggtcaat gttggtnggc tgattggtgg aaagtanggt ggaccaaagg 300
aagncncgtg agcagncanc nccagttctg caccagcagc gcctccgtcc tactnggggtg 360
ttcngtttct tcctggccct gngtgggcta nggctgatt cggaanatg cctttgcang 420
gaaggganga taantgggat ctaccaattg attctggcaa aacnatntct aagattnttn 480
tgctttatgt ggganacana tctanctctc atttnttgcg gnanatnaca ccctactcgt 540
gntcgancnc gtcttcgatt ttcgganaca cnccantnaa tactggcggt ctgttggtta 600
aaaaaaaaaa .aaaa                                     614

```

<210> 36
 <211> 686
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 222, 224, 237, 264, 285, 548, 551, 628, 643, 645, 665, 674
 <223> n = A,T,C or G

```

<400> 36
gtggctggcc cggttctccg cttctcccca tcccctactt tcctccctcc ctccctttcc 60
ctccctcgtc gactgttgct tgctggctgc agactccctg acccctccct caccctccc 120
taacctcggg gccaccggat tgcccttctt ttccctgttg ccagcccagc cctagtgtca 180
ggcggggggc ctggagcagc ccgaggcact gcagcagaag ananaaaaga cacgacnaac 240
ctcagctcgc cagtcgggtc gctngcttcc cgccgcatgg caatnagaca gacgcgctc 300
acctgctctg ggcacacgcg acccgtggtt gatttggcct tcagtggcat cacccttatg 360
ggtatttctt aatcagcgct tgcaaagatg gttaacctat gctacgccag ggagatacac 420
gagactggat tggaacattt ttggggctca aaggctctgt tgggggtgca cactgaataa 480
ggatgccacc aaagcagcta cagcagctgc agatttcaca gccaagtgt gggaatgct 540
ctcagganat naattgataa cctggctcat aacacattgt caagaatgt gatttcccca 600
ggatattatt atttgtttac cggggganag gataactgtt tcncntatth taattgaaca 660
aactnaaaca aaanctaagg aaatcc                                     686

```

<210> 37
 <211> 681

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 7, 10, 11, 19, 25, 32, 46, 53, 77, 93, 101, 103, 109, 115,
123, 128, 139, 157, 175, 180, 192, 193, 194, 212, 218, 226,
227, 233, 240, 241, 259, 260, 267, 289, 296, 297, 298, 312,
313, 314, 320, 325, 330, 337, 345, 346, 352, 353, 356
<223> n = A,T,C or G

<221> misc_feature

<222> 382, 385, 400, 427, 481, 484, 485, 491, 505, 515, 533, 542,
544, 554, 557, 560, 561, 564, 575, 583, 589, 595, 607, 619,
628, 634, 641, 645, 658, 670
<223> n = A,T,C or G

<400> 37

```
gagacanacn naacgtcang agaanaaaag angcatggaa cacaanccag gcncgatggc 60
caccttccca ccagcancca gcgcccccca gcngccccca ngnccggaag accangactc 120
cancctgnat caatctganc tctattcctg gcccatncct acctcggaag tggangccgn 180
aaaggctcgca cnnncagaga agctgctgcc ancaccancc gccccnccc tgcgaggctn 240
nataggaaac tggtagaccn gctgcanaat tcatacagga gcacgcgag ggcacnnnct 300
cacactgagt tnnngatgan gcctnaccan ggacctnccc cagcnnattg annacnggac 360
tgcgaggagaa ggaagacccc gnacnggatc ctggcggcgn tgccaccccc ccaccctag 420
gattatnccc cttgactgag tctctgaggg gctaccgaa cccgcctcca ttcctacca 480
natnntgctc natcgggact gacangctgg ggatnggagg ggctatcccc cancatcccc 540
tnanaccaac agcnaacngan natnggggct ccccnngggtc ggngcaacnc tcctncccc 600
cggcgcnngc cttcggtgnt gtccctccntc aacnaattcc naaanggcgg gccccccngt 660
ggactcctcn ttgttccctc c                                     681
```

<210> 38

<211> 687

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 3, 30, 132, 151, 203, 226, 228, 233, 252, 264, 279, 306,
308, 320, 340, 347, 380, 407, 429, 437, 440, 445, 448, 491,
559, 567, 586, 589, 593, 596, 603, 605, 606, 609, 626, 639,
655, 674, 682
<223> n = A,T,C or G

<400> 38

```
canaaaaaaa aaacatggc cgaaccagn aagctgcgcg atggcgccac ggcccctctt 60
ctcccgccct gtgtccggaa ggtttccctc cgaggcgccc cggctcccgc aagcggagga 120
gagggcgga cntgccggg ccggagctca naggccctgg ggccgctctg ctctcccgcc 180
atcgcaagg cgcgctaac ctnaggcctc cccgcaaagg tcccnangc ggnggcggcg 240
gggggctgtg anaaccgcaa aaanaacgct gggcgcgeng cgaaccgctc ccccccgcg 300
aaggananac ttccacagan gcagcgttcc cacagccan agccacnttt ctagggtgat 360
gcaccccgagt aagttcctgn cggggaagct caccgctgtc aaaaaanctc ttcgctccac 420
cggcgcacna agggggangan ggcangangc tgccgcccgc acaggctcgc tgatcacgctc 480
gcccgcccta ntctgctttt gtgaatctcc actttgttca accccaccgc ccgttctctc 540
ctccttgccg cttcctctna ccttaanaac cagcttctc taccnatng tanttctct 600
gcncnngtng aaattaattc ggtccnccgg aacctcttnc ctgtggcaac tgctnaaaga 660
aactgctgtt ctgnttactg cngtccc                                     687
```

<210> 39
<211> 695
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 300, 401, 423, 429, 431, 437, 443, 448, 454, 466, 492, 515,
523, 524, 536, 538, 541, 552, 561, 566, 581, 583, 619, 635,
636, 641, 649, 661, 694
<223> n = A,T,C or G

<400> 39
actagtctgg cctacaatag tgtgattcat gtaggacttc tttcatcaat tcaaaacccc 60
tagaaaaacg tatacagatt atataagtag ggataagatt tctaacattt ctgggctctc 120
tgaccctgc ctagactgt ggaaaggag tattattata gtatacaaca ctgctgttgc 180
cttattagtt ataacatgat aggtgctgaa ttgtgattca caatttaaaa aactgtaat 240
ccaaactttt ttttttaact gtagatcatg catgtgaatg ttaatgttaa tttgttcaan 300
gttgttatgg gtagaaaaaa ccaatgcct taaaatttta aaaagcaggg cccaaactta 360
ttagtttaaa attaggggta tgtttccagt ttgttattaa ntggttatag ctctgtttag 420
aanaaatcna ngaacangat ttngaaantt aagntgacat tatttnccag tgacttgta 480
atttgaaatc anacacggca ccttccggtt tggtnctatt ggnntttgaa tccaancngg 540
ntccaaatct tnttgaaac ngtcnntta acttttttac nanatcttat ttttttattt 600
tggaatggcc ctatttaang ttaaaagggg ggggnccac naccattcnt gaataaaact 660
naatatatat ccttggtccc ccaaaattta agngg 695

<210> 40
<211> 674
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 403, 428, 432, 507, 530, 543, 580, 583, 591, 604, 608, 621,
624, 626, 639, 672
<223> n = A,T,C or G

<400> 40
actagtagtc agttgggagt ggttgctata ccttgacttc atttatatga atttcactt 60
tattaaataa tagaaaagaa aatcccgggtg cttgcagtag agttatagga cattctatgc 120
ttacagaaaa tatagccatg attgaaatca aatagtaaag gctgttctgg ctttttatct 180
tcttagctca tcttaaataa gtagtacact tgggatgcag tgcgtctgaa gtgctaataca 240
gttgtaacaa tagcacaat cgaacttagg atgtgttct tctcttctgt gtttcgattt 300
tgatcaattc ttttaatttg ggaacctata atacagtttt cctattcttg gagataaaaa 360
ttaaatggat cactgatatt taagtcattc tgcttctcat ctnaatattc catattctgt 420
attagganaa antacctccc agcacagccc cctctcaaac cccacccaaa accaagcatt 480
tggaatgagt ctcttttatt tccgaantgt ggatggtata acccatatcn ctccaatttc 540
tgnttgggtt gggtattaat ttgaactgt catgaaaagn ggnaatcttt nctttgggtc 600
aaantttnc ggtaatttg nctngncaaa tccaatttnc ttttaagggtg tctttataaa 660
atttgctatt cngg 674

<210> 41
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> 243, 247, 251, 261, 267, 272, 298, 312, 315, 421, 432, 434,
501, 524, 569, 594, 607, 650
<223> n = A,T,C or G

<400> 41

```
gaaacatgca agtaccacac actgtttgaa ttttgacaaa aaagtgactg tagggatcag 60
gtgatagccc cggaatgtac agtgtcttgg tgcaccaaga tgccttctaa aggctgacat 120
accttgggac cctaattggg cagagagtat agccctagcc cagtgggtgac atgaccactc 180
cctttgggag gctgaagtta aagggaatgg tatgtgtttt ctcatggaag cagcacatga 240
atnggtnaca ngatgttaaa ntaaggntct antttgggtg tcttgtcatt tgaaaaantg 300
acacactcct ancanctggt aaagggtgac tggagccat ggaagaactc taaaaacatt 360
agcatgggct gatctgatta cttcctggca tcccgctcac ttttatggga agtcttatta 420
naaggatggg ananttttcc atatccttgc tgttggaaact ctggaacact ctctaaattt 480
ccctctatta aaaatcactg nccttactac acttcctcct tgganggaata gaaatggacc 540
tttctctgac ttagttcttg gcatggganc cagcccaaact taaaatctga cttntccggt 600
ttctccngaa ctcacctact tgaattggtg aaacctcctt tggaattagn aaaaacc 657
```

<210> 42

<211> 389

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 179, 317, 320

<223> n = A,T,C or G

<400> 42

```
actagtgtcg aggaatgtaa acaagtttgc tgggccttgc gagacttcac caggttgttt 60
cgatagctca cactcctgca ctgtgcctgt caccaggaa tgcctttttt aattagaaga 120
caggaagaaa acaaaaacca gactgtgtcc cacaatcaga aacctccgtt gtggcagang 180
ggccttcacc gccaccaggg tgtcccgcca gacagggaga gactccagcc ttctgaggcc 240
atcctgaaga attcctgttt gggggttgtg aaggaaaatc acccggtatt aaaaagatgc 300
tggtgcctgc ccgcgtngtn gggaagggac tgggtttcctg gtgaatttct taaaagaaaa 360
atattttaag ttaagaaaaa aaaaaaaaaa 389
```

<210> 43

<211> 279

<212> DNA

<213> Homo sapiens

<400> 43

```
actagtgaca agctcctggt cttgagatgt cttctcgtta aggagatggg ccttttggag 60
gtaaaggata aaatgaatga gttctgtcat gattcactat tctagaactt gcatgacctt 120
tactgtgtta gctccttgaa tgttcttgaa atttttagact ttctttgtta acaataata 180
tgtccttatc attgtataaa agctgttatg tgcaacagtg tggagatcct tgtctgattt 240
aataaaatac ttaaactact aaaaaaaaaa aaaaaaaaaa 279
```

<210> 44

<211> 449

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 245, 256, 264, 266, 273, 281, 323, 325, 337, 393

<223> n = A,T,C or G

```

<400> 44
actagtagca tcttttctac aacgttaaaa ttgcagaagt agcttatcat taaaaaacia 60
caacaacaac aataacaata aatcctaagt gttaatcagt tattctaccc cctaccaagg 120
atatcagcct gttttttccc ttttttctcc tgggaataat tgtgggcttc ttcccaaatt 180
tctacagcct ctttctctct ctcatgcttg agcttccctg tttgcacgca tgcgttgtgc 240
aagantgggc tgtttngctt ggantncggt ccnagtggaa ncatgcttcc ccttgttact 300
gttgaagaa actcaaacct tcnancccta ggtgttncca ttttgtcaag tcatcactgt 360
atttttgtac tggcattaac aaaaaaagaa atnaaatatt gttccattaa actttaataa 420
aactttaaaa gggaaaaaaa aaaaaaaa 449

```

```

<210> 45
<211> 559
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 263
<223> n = A,T,C or G

```

```

<400> 45
actagtgtgg gggaatcacg gacacttaaa gtcaatctgc gaaataattc ttttattaca 60
cactcactga agtttttgag tcccagagag ccattctatg tcaaacattc caagtactct 120
ttgagagccc agcattacat caacatgccc gtgcagttca aaccgaagtc cgcaggcaaa 180
tttgaagctt tgcttgtcat tcaaacagat gaaggcaaga gtattgctat tcgactaatt 240
ggtgaagctc ttggaaaaaa ttactagaa tactttttgt gttaagttaa ttacataagt 300
tgtattttgt taactttatc tttctacact acaattatgc ttttgtatat atattttgta 360
tgatggatat ctataattgt agattttgtt tttaacaagct aatactgaag actcgactga 420
aatattatgt atctagccca tagtattgta cttaactttt acaggggtgaa aaaaaaattc 480
tgtgtttgca ttgattatga tattctgaat aaatatggga atatatttta atgtgggtaa 540
aaaaaaaaaa aaaaaggaa 559

```

```

<210> 46
<211> 731
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 270, 467, 477, 502, 635, 660, 671, 688, 695, 697, 725
<223> n = A,T,C or G

```

```

<400> 46
actagttcta gtaccatggc tgtcatagat gcaaccatta tattccattt agtttcttcc 60
tcaggttccc taacaattgt ttgaaactga atatatatgt ttatgtatgt gtgtgtgttc 120
actgtcatgt atatggtgta tatgggatgt gtgcagtttt cagttatata tatattcata 180
tatacatatg catatatatg tataatatac atatatacat gcatacactt gtataatata 240
catatatata cacatatatg cacacatatn atcactgagt tccaaagtga gtctttattt 300
ggggcaattg tattctctcc ctctgtctgc tcaactggcc tttgcaagac atagcaattg 360
cttgatttcc tttggataag agtcttatct tcggcactct tgactctagc cttaacttta 420
gatttctatt ccagaatacc tctcatatct atcttaaaac ctaaganggg taaagangtc 480
ataagattgt agtatgaaag antttgctta gttaaattat atctcaggaa actcattcat 540
ctacaaatta aattgtaaaa tgatggtttg ttgtatctga aaaaatgttt agaacaagaa 600
atgtaactgg gtacctgtta tatcaaagaa cctcnattta ttaagtctcc tcatagccan 660
atccttatat ngccctctct gacctgantt aatananact tgaataatga atagttaatt 720
taggnntggg c 731

```

```

<210> 47

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<211> 640
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 5, 28, 106, 153, 158, 173, 176, 182, 189, 205, 210, 214,
225, 226, 229, 237, 260, 263, 269, 277, 281, 282, 322, 337,
338, 354, 365, 428, 441, 443, 456, 467, 476, 484, 503, 508,
554, 567, 575, 579, 588, 601, 606, 609, 611, 621, 636
<223> n = A,T,C or G

<400> 47
tgcgngccgg tttggccctt ctttgtanga cactttcatc cgccctgaaa tcttcccgat 60
cgtaataaac tcctcaggtc cctgcctgca cagggttttt tcttantttg ttgcctaaca 120
gtacaccaa tgtgacatcc tttcaccaat atngatttct tcataccaca tcntcnatgg 180
anacgactnc aacaattttt tgatnaccn aaanactggg ggctnnaana agtacantct 240
ggagcagcat ggacctgtcn gcnactaang gaacaanagt nntgaacatt tacacaacct 300
ttggatatgtc ttactgaaag anagaaacat gcttctnncc ctgaccacg aggncaaccg 360
caganattgc caatgccaaag tccgagcggg tagatcaggt aatacattcc atggatgcat 420
tacatacnnt gtccccgaaa nanaagatgc cctaanggct tcttcanact ggtccngaaa 480
acanctacac ctggtgcttg ganaacanac tctttggaag atcatctggc acaagttccc 540
cccagtgggg tttnccttg cacttanctt accanatcna ttcggaancc attctttgcc 600
ntggcnttnt nttgggacca ntcttctcac aactgnacce 640

<210> 48
<211> 257
<212> DNA
<213> Homo sapiens

<400> 48
actagtatat gaaaatgtaa atatcacttg tgtaactcaa caaaagttgg tcttaagctt 60
ccaccttgag cagccttgga aacctaacct gcctctttta gcataatcac attttctaaa 120
tgattttctt tgttcctgaa aaagtgattt gtattagttt tacatttgtt ttttggaga 180
ttatatttgt atatgtatca tcataaaata tttaaataaa agtatctttt agagtgaana 240
aaaaaaaaaa aaaaaaa 257

<210> 49
<211> 652
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 410, 428, 496, 571, 647
<223> n = A,T,C or G

<400> 49
actagttcag atgagtggct gctgaagggg cccccttgct attttcatta taaccaatt 60
tccacttatt tgaactctta agtcataaat gtataatgac ttatgaatta gcacagttaa 120
gttgacacta gaaactgcc atttctgtat tacactatca aataggaaac attggaaaga 180
tggggaaaaa aatcttattt taaaatggct tagaaagttt tcagattact ttgaaaattc 240
taaacttctt tctgtttcca aaacttgaaa atatgtagat ggactcatgc attagactg 300
ttttcaaagc tttcctcaca tttttaaagt gtgattttcc ttttaataa catatttatt 360
ttctttaagc cagctatatc ccaacccatg actttggaga tatacctatn aaaccaatat 420
aacagcangg ttattgaagc agcttttctca aatgttgctt cagatgtgca agttgcaaat 480
tttattgtat ttgtanaata caatttttgt tttaaactgt atttcaatct atttctccaa 540
gatgcttttc atatagagtg aaatatccca ngataactgc ttctgtgtcg tcgcatttga 600

cgcataactg cacaaatgaa cagtgtatac ctcttggttg tgcattnacc cc 652

<210> 50

<211> 650

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 237, 270, 311, 443, 454, 488, 520, 535, 539, 556, 567, 594, 603, 634

<223> n = A,T,C or G

<400> 50

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ttgcgctttg atttttttag ggcttgtgcc ctgtttcact tatagggtct agaatgcttg 60
tgttgagtaa aaaggagatg cccaatattc aaagctgcta aatgttctct ttgccataaa 120
gactccgtgt aactgtgtga acacttgga tttttctcct ctgtcccag gtcgtcgtct 180
gctttctttt ttgggttctt tctagaagat tgagaaatgc atatgacagg ctgagancac 240
ctcccaaac acacaagctc tcagccacan gcagcttctc cacagcccca gtttcgcaca 300
ggctcctgga nggctgcctg ggggaggcag acatgggagt gccaagggtg ccagatggtt 360
ccaggactac aatgtcttta tttttaactg tttgccactg ctgccctcac ccctgcccg 420
ctctggagta ccgtctgccc canacaagtg ggantgaaat gggggtgggg gggaacactg 480
attccantt agggggtgcc taactgaaca gtagggatan aagggtgtgaa cctgngaant 540
gcttttataa attatnttcc ttgttanatt tatttttta ttaatctct gttnaactgc 600
ccngggaaaaa ggggaaaaaa aaaaaaaat tctntttaaa cacatgaaca 650

```

<210> 51

<211> 545

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 66, 159, 195, 205, 214, 243, 278, 298, 306, 337, 366, 375, 382, 405, 446, 477, 492, 495, 503, 507, 508, 521, 537

<223> n = A,T,C or G

<400> 51

```

tggcgtgcaa ccagggtagc tgaagtttgg gtctgggact ggagattggc cattaggcct 60
cctganattc cagctccctt ccaccaagcc cagtcttgct acgtggcaca gggcaaacct 120
gactcccttt gggcctcagt ttcccctccc ctcatgana tgaaaagaat actactttt 180
cttgttggtc taacnttgct ggacncaaag tgtngtcatt attgttgtat tgggtgatgt 240
gtncaaaact gcagaagctc actgcctatg agaggaanta agagagatag tggatganag 300
ggacanaagg agtcattatt tggatatagat ccaccntcc caacctttct ctctcagtc 360
cctgcncctc atgtntctgg tntggtgagt cctttgtgcc accanccatc atgctttgca 420
ttgctgccat cctgggaagg gggtnatcg tctcacaact tgttgtcatc gtttganatg 480
catgctttct tnatnaaaca aanaaannaa tgtttgacag ngtttaaaat aaaaaanaa 540
caaaa 545

```

<210> 52

<211> 678

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 98, 119, 121, 131, 136, 139, 140, 142, 143, 163, 168, 172, 176, 184, 189, 190, 191, 200, 201, 205, 207, 221, 223, 229,

230, 237, 240, 241, 255, 264, 266, 267, 276, 280, 288, 289,
291, 297, 301, 306, 308, 314, 315, 326, 332, 335, 337
<223> n = A,T,C or G

<221> misc_feature

<222> 339, 341, 343, 344, 345, 347, 350, 355, 356, 358, 362, 363,
372, 379, 395, 397, 398, 400, 403, 412, 414, 421, 423, 431,
435, 438, 439, 450, 457, 463, 467, 471, 474, 480, 483, 484,
487, 490, 491, 492, 493, 499, 500, 504, 508, 518, 536
<223> n = A,T,C or G

<221> misc_feature

<222> 538, 549, 551, 552, 554, 556, 557, 562, 563, 567, 571, 572,
576, 579, 590, 592, 595, 598, 606, 609, 613, 620, 622, 624,
626, 631, 634, 638, 641, 647, 654, 660, 661, 674
<223> n = A,T,C or G

<400> 52

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actagtagaa gaactttgcc gcttttgtgc ctctcacagg cgcctaaagt cattgccatg 60
ggaggaagac gatttggggg gggagggggg gggggcangg tccgtggggc ttccctant 120
ntatctccat ntccantggn cnntgtcgcc tcttccctcg tcncattnga anttantccc 180
tggnccccnn nccctctccn nccnncnct ccccccctcg ncnccctcnn cttttntan 240
ncttccccat ctccntcccc cctnanngtc ccaacnccgn cagcaatnnc ncacttnctc 300
nctccncccc tccnncggtt cttctnttct cnacntntnc ncnntnccn tgccnntnaa 360
annctctccc cnetgcaanc gattctctcc ctccnccnnc ctnctccact cntncttctc 420
ncnccgtcct ntntctcnn ccacctctcn ccttcgnccc cantacnctc nccncccttn 480
cgnntcttn nnntcctcnn accncccccc tcccttcccc cctcttctcc ccggtntntc 540
tctctccccc nncnncnct cnncccntcc nngcgnccnt ttccgccccn cncnccntt 600
ccttctctnc cantccatcn cntntnccat nctnccctncc nctcacnccc gctncccccn 660
ntctctttca cacngtcc 678
```

<210> 53

<211> 502

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 139, 146, 215, 217, 257, 263, 289, 386, 420, 452, 457, 461,
466, 482, 486

<223> n = A,T,C or G

<400> 53

```
tgaagatcct ggtgtcgcca tgggcccgcg ccccgcccgt tgttaccggt attgtaagaa 60
caagccgtac ccaaagtctc gcttctgccg aggtgtccct gatgccaaaa ttcgcathtt 120
tgacctgggg cggaaaaang caaaantgga tgagtctccg ctttgtggcc acatggtgtc 180
agatcaatat gagcagctgt cctctgaagc cctgnangct gcccgaaatt gtgccaataa 240
gtacatggta aaaagtngtg gcnaagatgc ttccatatcc ggggtgcggnt ccaccccttc 300
cacgtcatcc gcatcaacaa gatgttgtcc tgtgctgggg ctgacaggct cccaacaggc 360
atgcgaagtg cctttggaaa acccanggca ctgtggccag gggttcacatt ggccaattn 420
atcatgttca tccgcaccaa ctgcagaaca angaantgt naattnaagc cctgcccagg 480
gncaanttca aatttcccgg cc 502
```

<210> 54

<211> 494

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> 431, 442, 445
 <223> n = A,T,C or G

<400> 54
 actagtccaa gaaaaatatg cttaatgtat attacaaagg ctttgtatat gttaacctgt 60
 tttaatgccaa aaagtttgct ttgtccacaa tttccttaag acctcttcag aaagggattt 120
 gtttgcctta atgaatactg ttgggaaaaa acacagtata atgagtgaag agggcagaag 180
 caagaaattt ctacatctta gcgactccaa gaagaatgag tatccacatt tagatggcac 240
 attatgagga ctttaaatctt tccttaaaca caataatggt ttcttttttc ttttattcac 300
 atgatttcta agtatatttt tcatgcagga cagtttttca accttgatgt acagtgactg 360
 tgttaaattt ttctttcagt ggcaacctct ataatcttta aaatatgggt agcatcttgt 420
 ctgttttgaa ngggatatga cnatnaatct atcagatggg aaatcctgtt tccaagttag 480
 aaaaaaaaaa aaaa 494

<210> 55
 <211> 606
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 375, 395, 511, 542, 559, 569, 578, 581
 <223> n = A,T,C or G

<400> 55
 actagtaaaa agcagcattg ccaaataatc cctaattttc cactaaaaat ataatgaaat 60
 gatgttaagc tttttgaaaa gtttaggtta aacctactgt tgtagatta atgtatttgt 120
 tgcttccctt tatctggaat gtggcattag cttttttatt ttaacctct ttaattctta 180
 ttcaattcca tgacttaagg ttggagagct aaacactggg atttttggat aacagactga 240
 cagttttgca taattataat cggcattgta catagaaagg atatggctac cttttgttaa 300
 atctgcactt tctaaatata aaaaaaggga aatgaagtat aaatcaattt ttgtataatc 360
 tgtttgaaac atgantttta tttgcttaat attanggctt tgcccttttc tgtagtctc 420
 ttgggatcct gtgtaaaact gttctcatta aacaccaaac agttaagtcc attctctggt 480
 actagctaca aattccggtt catattctac ntaacaattt aaattaactg aaatatttct 540
 anatggtcta cttctgtcnt ataaaaacna aacttgantt nccaaaaaaa aaaaaaaaaa 600
 aaaaaa 606

<210> 56
 <211> 183
 <212> DNA
 <213> Homo sapiens

<400> 56
 actagtatat ttaaacttac aggcttattt gtaatgtaaa ccaccatttt aatgtactgt 60
 aattaacatg gttataatac gtacaatcct tccctcatcc catcacacaa ctttttttgt 120
 gtgtgataaa ctgatttttg tttgcaataa aaccttgaaa aataaaaaaa aaaaaaaaaa 180
 aaa 183

<210> 57
 <211> 622
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 358, 368, 412, 414, 425, 430, 453, 455, 469, 475, 495, 499,

529, 540, 564, 575, 590
 <223> n = A,T,C or G

<400> 57

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actagtcact actgtcttct ccttgtagct aatcaatcaa tattcttccc ttgcctgtgg 60
gcagtggaga gtgctgctgg gtgtacgctg cacctgcccc ctgagttggg gaaagaggat 120
aatcagttag cactgttctg ctgagagctc ctgatctacc ccaccccta ggatccagga 180
ctgggtcaaa gctgcatgaa accaggccct ggcagcaacc tgggaatggc tggaggtggg 240
agagaacctg acttctcttt ccctctccct cctccaacat tactggaact ctatcctgtt 300
agggatcttc tgagcttggt tccctgctgg gtgggacaga agacaaagga gaagggangg 360
tctacaanaa gcagcccttc tttgtcctct ggggttaatg agcttgacct ananttcatt 420
gaganaccan aagcctctga tttttaattt ccntnaaatg tttgaagtnt atatntacat 480
atatatatat cttttnaatnt ttgagtcctt gatatgtctt aaaatccant ccctctgccn 540
gaaacctgaa ttaaaacat gaanaaaat gtttncctta aagatgttan taattaattg 600
aaacttgaaa aaaaaaaaaa aa
```

622

<210> 58

<211> 433

<212> DNA

<213> Homo sapiens

<400> 58

```
gaacaaattc tgattggtta tgtaccgtca aaagacttga agaaatttca tgattttgca 60
gtgtggaagc gttgaaaatt gaaagtact gcttttccac ttgctcatat agtaaagggg 120
tcctttcagc tgccagtgtt gaataatgta tcatccagag tgatgttata tgtgacagtc 180
accagcttta agctgaacca ttttatgaat accaaataaa tagacctctt gtactgaaaa 240
catatttggt actttaatcg tgctgcttgg atagaaatat ttttactggg tcttctgaat 300
tgacagttaa cctgtccatt atgaatggcc tactgttcta ttatttggtt tgacttgaat 360
ttatccacca aagacttcat ttgtgtatca tcaataaagt tgtatgtttc aactgaaaaa 420
aaaaaaaaaa aaa
```

433

<210> 59

<211> 649

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 22, 190, 217, 430, 433, 484, 544, 550, 577, 583, 594

<223> n = A,T,C or G

<400> 59

```
actagttatt atctgacttt cnggttataa tcatttcta gagtgtgaag tagcctctgg 60
tgtcatttgg atttgcattt ctctgatgag tgatgctatc aagcaccttt gctgggtgctg 120
ttggccatat gtgtatgttc cctggagaag tgtctgtgct gagccttggc ccacttttta 180
attaggcgtn tgccttttta ttactgagtt gtaaganttc tttatatatt ctggattcta 240
gacccttata agatacatgg ttgcaaata ttttctccca ttctgtgggt tgtgttttca 300
ctttatcgat aatgtcctta gacatataat aaatttgat tttaaaagt acttgatttg 360
ggctgtgcaa ggtgggctca cgcttgtaat ccagcactt tgggagactg aggtgggtgg 420
atcatatgan gangctagga gtgcagggtc agcctggcca gcatagcgaa aacttgtctc 480
tacnaaaaat acaaaaatta gtcaggcatg gtggtgcacg tctgtaatac cagcttctca 540
ggangctgan gcacaaggat cacttgaacc ccagaangaa gangttgcag tganctgaag 600
atcatgccag ggcaacaaaa atgagaactt gtttaaaaaa aaaaaaaaaa
```

649

<210> 60

<211> 423

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> 209, 222, 277, 389, 398
<223> n = A,T,C or G

<400> 60
actagttcag gccttccagt tcaactgacaa acatggggaa gtgtgcccag ctggctggaa 60
acctggcagt gataccatca agcctgatgt ccaaaagagc aaagaatatt tctccaagca 120
gaagtgagcg ctgggctgtt ttagtgccag gctgcggtgg gcagccatga gaacaaaacc 180
tcttctgtat tttttttttc cattagtana acacaagact cngattcagc cgaattgtgg 240
tgtcttaāaa ggcagggtct tctacaggg ggtgganaaa acagcctttc ttccttttgt 300
aggaatggcc tgagttggcg ttgtgggcag gctactggtt tgtatgatgt attagtagag 360
caaccatta atcttttcta gtttgtatna aacttganct gagaccttaa acaaaaaaaa 420
aaa 423

<210> 61
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 195, 285, 295, 329, 335, 340, 347, 367, 382, 383, 391, 396,
418
<223> n = A,T,C or G

<400> 61
cgggactgga atgtaaagtg aagttcggag ctctgagcac gggctcttcc cgccgggtcc 60
tccctcccca gacccagag ggagaggccc accccgcccā gcccgcctcc agcccctgct 120
caggtctgag tatggctggg agtcgggggc cacaggcctc tagctgtgct gctcaagaag 180
actggatcag ggtanctaca agtggccggg ccttgccctt gggattctac cctgttccta 240
atttggtgtt ggggtgcggg gtccctggcc cctttttcca cactncctcc ctccngacag 300
caacctccct tggggcaatt gggcctggnt ctccnccgn tggtgcnacc ctttgttgg 360
ttaaggnctt taaaaatgtt annttttccc ntgccnggt taaaaaagga aaaaactnaa 420
aaa 423

<210> 62
<211> 683
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 218, 291, 305, 411, 416, 441, 443, 453, 522, 523, 536, 542,
547, 566, 588, 592, 595, 603, 621, 628, 630, 632, 644, 645,
648, 655, 660, 672, 674, 676, 677, 683
<223> n = A,T,C or G

<400> 62
gctggagagg ggtacggact ttcttgaggt tgtcccaggt tggaatgaga ctgaactcaa 60
gaagagaccc taagagactg gggaatggtt cctgccttca ggaaagtgaā agacgcttag 120
gctgtcaaca cttaaaggaa gtccccttga agcccagagt ggacagacta gaccattga 180
tggggccact ggccatggc cgtggacaag acattccngt gggccatggc acaccggggg 240
ggatcaaaat gtgtacttgt ggggtctcgc cccttgccaa aaccaaacca ntccactcc 300
tgtcnttgaā ctttcttccc attccctcct ccccaaatgc acttcccctc ctccctctgc 360
ccctcctgtg tttttggaat tctgtttccc tcaaaattgt taatttttta nttttngacc 420
atgaacttat gtttggggtc nangttcccc ttnccaatgc atactaatat attaatggtt 480

atttattttt gaaatatttt ttaatgaact tggaaaaaat tnntggaatt tccttncttc 540
cntttntttt ggggggggtg gggggntggg ttaaaatttt ttggaancc cnatnggaaa 600
ttnttacttg gggccccctt naaaaaantn anttccaatt cttnnatngc ccctnttccn 660
ctaaaaaaa ananannaaa aan 683

<210> 63

<211> 731

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 237, 249, 263, 288, 312, 317, 323, 326, 337, 352, 362, 370,
377, 400, 411, 414, 434, 436, 446, 457, 473, 486, 497, 498,
502, 512, 531, 546, 554, 563, 565, 566, 588, 597, 608, 611,
613, 615, 627, 632, 640, 641, 644, 654, 660, 663, 665
<223> n = A,T,C or G

<221> misc_feature

<222> 671, 678, 692, 697, 698, 699, 704, 705, 712, 714, 717, 718,
719, 723, 725, 730, 731

<223> n = A,T,C or G

<400> 63

actagtcata aagggtgtgc gcgtcttcga cgtggcggtc ttggcgccac tgctgcgaga 60
cccggccctg gacctcaagg tcatccactt ggtgcgtgat cccgcgcggg tggcgagttc 120
acggatccgc tcgcgccacg gcctcatccg tgagagccta cagggtggtgc gcagccgaga 180
ccgcgagctc accgcatgcc cttcttgtag gccgcgggcc acaagcttgg cgcccanaaa 240
gaaggcgtn ggggcccgca aantaccacg ctctgggcgc tatggaangt cctcttgcaa 300
taatatgggt tnaaaanctg canaanagcc cctgcacccc cctgaactgg gntgcagggc 360
cncttacctn gtttggnctg gggtacaaag aacctgtttn ggaaaaccct nccnaaaacc 420
ttccgggaaa attntncaaa ttttntttgg ggaattnttg ggtaaacccc ccnaaaatgg 480
gaaacntttt tgccctnnaa antaaaccat tnggttccgg gggccccccc ncaaaaccct 540
ttttntttt tttntgcccc cantnncccc ccggggcccc ttttttngg ggaaaanccc 600
ccccctncc nanantttta aaaggngggg anaatttttn nttnccccc gggnccccc 660
ggngntaaaa nggtttcncc ccccgaggg gnggggnnnc ctcnnaaacc cntntcnna 720
ccncttttn n 731

<210> 64

<211> 313

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 240

<223> n = A,T,C or G

<400> 64

actagttgtg caaaccacga ctgaagaaag acgaaaagtg ggaaataact tgcaacgtct 60
gttagagatg gttgctacac atgttggtgc ttagagaaaa catcttgagg agcagattgc 120
taaagttgat agagaatatg aagaatgcat gtcagaagat ctctcggaat atattaaaga 180
gattagagat aagtatgaga agaaagctac tctaattaag tcttctgaag aatgaagatn 240
aaatgttgat catgtatata tatccatagt gaataaaatt gtctcagtaa agttgtaaaa 300
aaaaaaaaaaa aaa 313

<210> 65

<211> 420

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 400, 402, 403, 404, 405, 406, 409, 411, 412, 414, 415, 416

<223> n = A,T,C or G

<400> 65

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actagttccc tggcaggcaa gggcttccaa ctgaggcagt gcatgtgtgg cagagagagg 60
caggaagctg gcagtggcag cttctgtgtc tagggagggg tgtgggtccc tccttccttg 120
tctgggaggt tggagggaag aatctaggcc ttagcttgcc ctccgtccac ccttcccctt 180
gtagatactg ccttaacact ccctcctctc tcagctgtgg ctgccacca agccagggtt 240
ctccgtgctc actaatttat ttccaggaaa ggtgtgtgga agacatgagc cgtgtataat 300
atttgtttta acattttcat tgcaagtatt gaccatcatc cttggttggt tatcgttgta 360
acacaaatta atgatattaa aaagcatcca aacaaagccn annnnnaana nnannngaaa 420
```

<210> 66

<211> 676

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 328, 454, 505, 555, 586, 612, 636, 641

<223> n = A,T,C or G

<400> 66

```
actagtttcc tatgatcatt aaactcattc tcagggttaa gaaaggaatg taaatttctg 60
cctcaatttg tacttcatca ataagttttt gaagagtgcg gatttttagt caggtcttaa 120
aaataaactc acaaattctgg atgcatttct aaattctgca aatgtttcct ggggtgactt 180
aacaaggaat aatcccacaa tatacctagc tacctaatac atggagctgg ggctcaaccc 240
actgttttta aggatttgcg cttacttggt gctgaggaaa aataagtagt tccgagggaa 300
gtagttttta aatgtgagct tatagatngg aaacagaata tcaacttaat tatggaaatt 360
gttagaaacc tgttctcttg ttatctgaat cttgattgca attactattg tactggatag 420
actccagccc attgcaaagt ctccagatgc ttanctgtgt agttgaattc cttggaaatt 480
ctttttaaga aaaaattgga gtttnaaaga aataaacccc tttgttaaata gaagcttggc 540
tttttggtga aaaanaatca tcccgagggg cttattgttt aaaaanggae ttttaagcct 600
ccctgaaaaa anttgtaaat taaatgggga aaatgntggg naaaaattat ccgttagggg 660
ttaaagggaa aactta 676
```

<210> 67

<211> 620

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 419, 493, 519, 568, 605, 610

<223> n = A,T,C or G

<400> 67

```
caccattaaa gctgcttacc aagaacttcc ccagcatttt gacttccttg tttgatagct 60
gaattgtgag caggtgatag aagagccttt ctagttgaac atacagataa tttgctgaat 120
acattccatt taatgaaggg gttacatctg ttacgaagct actaagaagg agcaagagca 180
taggggaaaa aaatctgatc agaacgcac aaactcacat gtgccccctc tactacaaac 240
agattgtagt gctgtggtgg tttattccgt tgtgcagaac ttgcaagctg agtcactaaa 300
```

cccaaagaga ggaaattata ggtagttaa acattgtaat ccaggaact aagttaatt 360
cacttttgaa gtgttttggt ttttattttt ggtagtctg atttactttg ggggaaaang 420
ctaaaaaaa agggatatca atctctaatt cagtgtccac taaaagttgt ccctaaaaag 480
tctttactgg aanttattggg actttttaag ctccaggtnt tttggtcctc caaattaacc 540
ttgcatgggc cccttaaaat tgttgaangg cattcctgcc tctaagtttg gggaaaattc 600
ccccnttttn aaaatttga 620

<210> 68

<211> 551

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 286, 464, 480, 501, 502, 518, 528, 533, 536, 537, 538, 539,
540, 541, 543, 544, 545, 547, 548, 549

<223> n = A, T, C or G

<400> 68

actagtagct ggtacataat cactgaggag ctatttctta acatgctttt atagaccatg 60
ctaagtctag accagtattt aagggtaat ctcacacctc cttagctgta agagtctggc 120
ttagaacaga cctctctgtg caataacttg tggccactgg aaatccctgg gccggcattt 180
gtattggggt tgcaatgact cccaagggcc aaaagagtta aaggcacgac tgggatttct 240
tctgagactg tggtgaaact ccttccaagg ctgagggggt cagtangtgc tctgggaggg 300
actcgacc accctgatat tcaacaagcc acttgaagcc caattataaa attgttattt 360
tacagctgat ggaactcaat ttgaaccttc aaaactttgt tagtttatcc tattatattg 420
ttaaaccctaa ttacatttgt ctacatttgg atttggttcc tgtngcatat gttttttcn 480
cctatgtgct cccctcccc nnatcttaat ttaaacnca attttgcnat tcncnnnnn 540
nanannnna a 551

<210> 69

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 235, 310, 323, 381

<223> n = A, T, C or G

<400> 69

cagaaatgga aagcagagtt ttcatttctg tttataaacg tctccaaaca aaaatggaaa 60
gcagagtttt cattaaatcc ttttaccttt ttttttctt ggtaatccc tcaataaaca 120
gtatgtggga tattgaatgt taaaggata ttttttcta ttatttttat aattgtacaa 180
aattaagcaa atgttaaaag ttttatatgc tttattaatg ttttcaaaag gtatnatata 240
tgtgatacat tttttaagct tcagttgctt gtcttctggt actttctgtt atgggctttt 300
ggggagccan aaaccaatct acnatctctt tttgtttgcc aggacatgca ataaaattta 360
aaaaataaat aaaaactatt nagaaattga aaaaaa 396

<210> 70

<211> 536

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 388, 446, 455

<223> n = A, T, C or G


```

<400> 70
actagtgcaa aagcaaatat aaacatcgaa aaggcggttcc tcacgttagc tgaagatattc 60
cttcgaaaga cccctgtaaa agagcccaac agtgaaaatg tagatatcag cagtgaggga 120
ggcgtgacag gctggaagag caaatgctgc tgagcattct cctgttccat cagttgccat 180
ccactacccc gttttctctt cttgctgcaa aataaaccac tctgtccatt tttaactcta 240
aacagatatt tttgtttctc atcttaacta tccaagccac ctattttatt tgttctttca 300
tctgtgactg cttgctgact ttatcataat tttcttcaaa caaaaaaatg tatagaaaaa 360
tcatgtctgt gacttcattt ttaaatgnta cttgctcagc tcaactgcat ttcagttggt 420
ttatagtcca gttcttatca acattnaaac ctatngcaat catttcaaat ctattctgca 480
aattgtataa gaataaaaagt tagaatttaa caattaaaaa aaaaaaaaaa aaaaaa 536

```

<210> 71

<211> 865

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 22, 35, 39, 56, 131, 138, 146, 183, 194, 197, 238, 269, 277,
282, 297, 316, 331, 336, 340, 341, 346, 349, 370, 376, 381,
382, 392, 396, 397, 401, 433, 444, 445, 454, 455, 469, 472,
477, 480, 482, 489, 497, 499, 511, 522, 526, 527

<223> n = A,T,C or G

<221> misc_feature

<222> 545, 553, 556, 567, 574, 580, 610, 613, 634, 638, 639, 663,
672, 689, 693, 694, 701, 704, 713, 723, 729, 732, 743, 744,
749, 761, 765, 767, 769, 772, 774, 780, 783, 788, 792, 803,
810, 824, 840, 848

<223> n = A,T,C or G

<400> 71

```

gacaaagcgt taggagaaga anagaggcag ggaanactnc ccaggcacga tggccncctt 60
cccaccagca accagcgcgc cccaccagcc cccaggcccg gacgacgaag actccatcct 120
ggattaatct nacctctntc gcctgnccca ttcctacctc ggaggtggag gccggaaagg 180
tcnccaccaag aganaaactg ctgccaaacac caaccgcccc agccttgcg ggcacganag 240
gaaactggtg accaatctgc agaattctna gaggaanaag cnaggggccc cgcgctnaga 300
cagagctgga tatgangcca gaccatggac nctacnccn ncaatncana cgggactgcg 360
gaagatggan gaccncgac nngatcaggc cngctnncca nccccccacc cctatgaatt 420
attcccgcgt aangaatctc tganngcctt ccannaaagc gcctcccnc cnaacgnaan 480
tncaacatng ggattanang ctgggaactg naaggggcaa ancctnnaat atccccagaa 540
acaanctctc ccnaanaaac tggggcncct catnggtggn accaactatt aactaaaccg 600
cacgccaagn aantataaaa ggggggcccc tccncggnng acccctttt gtcccttaat 660
ganggttatc cnccttgctg accatggtnc ccnnttctgt ntgnatgttt ccnctcccct 720
ccnctatnt cnagccgaac tcnnatttnc ccgggggtgc natcnantng tncnctttt 780
ttngttgncc cngccctttc cngcggaaacn cgtttccccc ttantaacgg caccgggggn 840
aagggtgntt ggccccctcc ctccc 865

```

<210> 72

<211> 560

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 83, 173, 183, 186, 209, 211, 215, 255, 321, 322, 323, 335,
344, 357, 361, 368, 394, 412, 415, 442, 455, 469, 472, 475,

487, 513, 522, 528, 531, 534, 546
<223> n = A,T,C or G

<400> 72

```
cctggacttg tcttggttcc agaacctgac gacccggcga cggcgacgtc tcttttgact 60
aaaagacagt gtccagtgtc ccngcctagg agtctacggg gaccgcctcc cgcgccgcca 120
ccatgccccaa cttctctggc aactggaaaa tcatccgac ggaaaacttc gangaattgc 180
tcnaantgct ggggggtgaat gtgatgctna ngaanattgc tgtggctgca gcgtccaagc 240
cagcagtgga gatcnaacag gagggagaca ctttctacat caaaacctcc accaccgtgc 300
gcaccacaaa gattaacttc nnngttgggg aggantttga ggancaaaact gtggatngga 360
ngcctgtnaa aacctgggtga aatgggagaa tganaataaa atggtctgtg ancanaaaact 420
cctgaaagga gaaggccccc anaactcctg gaccngaaaa actgaccnc cnatngggga 480
actgatnctt gaacctgaa cggggcgggat gancctttt tnttgcncnc naanggggtc 540
tttcntttc cccaaaaaaa                                     560
```

<210> 73

<211> 379

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 8, 17, 18, 21, 26, 29, 30, 32, 53, 56, 67, 71, 81, 102, 104,
111, 112, 114, 119, 122, 124, 125, 134, 144, 146, 189, 190,
214, 215, 219, 220, 235, 237, 246, 280, 288, 302, 310, 313,
319, 322, 343, 353, 354

<223> n = A,T,C or G

<400> 73

```
ctggggancc ggcggtnngc nccatntcnn gncgcgaagg tggcaataaa aanccnctga 60
aaccgcncaa naacatgcc naagatatgg acgaggaaga tngngctttc nngnacaanc 120
gnannagga acanaacaaa ctcnangagc tctcaagcta atgccgcggg gaaggggccc 180
ttggccacnn gtggaattaa gaaatctggc aaanngtann tgttccttgt gcctnangag 240
ataagnagacc ctttatttca tctgtattta aacctctctn ttccctgnca taacttcttt 300
tnccacgtan agntggaant anttgttgtc ttggactgtt gtncatttta gannaaactt 360
ttgtcaaaaa aaaaaataa                                     379
```

<210> 74

<211> 437

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 145, 355

<223> n = A,T,C or G

<400> 74

```
actagtccag actgccacgc caaccccaga aaatacccca catgccagaa aagtgaagtc 60
ctaggtgttt ccatctatgt ttcaatctgt ccatctacca ggcctcgcga taaaaacaaa 120
acaaaaaac gctgccaggt tttanaagca gttctgtgtc caaaaccatc aggatcctgc 180
caccagggtt cttttgaaat agtaccacat gtaaaaggga atttggtttt cacttcattc 240
aatcactgaa ttgtcaggct ttgattgata attgtagaaa taagtagcct tctgtttgtg 300
gaataagtta taatcagtat tcatctcttt gttttttgtc actcttttct ctctnattgt 360
gtcattttgt ctgtttgaaa aatatcttct ctataaaatt aaactaacct gccttaaaaa 420
aaaaaaaaa aaaaaaa                                     437
```

<210> 75

<211> 579
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 440, 513, 539, 551
<223> n = A,T,C or G

<400> 75
ctccgtcgcc gccagatga tgtgcggggc gccctccgcc acgcagccgg ccaccgccga 60
gacccagcac atcgccgacc aggtgaggtc ccagcttgaa gagaaagaaa acaagaagtt 120
ccctgtgttt aaggccgtgt cattcaagag ccaggtggtc gcggggacaa actacttcat 180
caaggtgcac gtgcggcgacg aggacttcgt acacctgcga gtgttccaat ctctccctca 240
tgaaaacaag cccttgacct tatctaacta ccagaccaac aaagccaagc atgatgagct 300
gacctatttc tgatcctgac tttggacaag gcccttcagc cagaagactg acaaagtcatt 360
cctccgtcta ccagagcgtg cacttgtgat cctaaaataa gcttcatctc cgggctgtgc 420
ccttgggggtg gaagggggcan gatctgcact gcttttgcatt ttctcttcct aaatttcatt 480
gtgttgattc ttctcttcca ataggtgatc ttnattactt tcagaatatt ttccaaatna 540
gatatatattt naaaatcctt aaaaaaaaaa aaaaaaaaaa 579

<210> 76
<211> 666
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 411, 470, 476, 491, 506, 527, 560, 570, 632, 636, 643, 650,
654, 658
<223> n = A,T,C or G

<400> 76
gtttatccta tctctccaac cagattgtca gtccttgag ggcaagagcc acagtatatt 60
tccctgtttc ttccacagtg cctaataata ctgtggaact aggttttaatt aatttttttaa 120
ttgatgttgt tatgggcagg atggcaacca gaccattgtc tcagagcagg tgctggctct 180
ttcctggcta ctccatgttg gctagcctct ggtaacctct tacttattat cttcaggaca 240
ctcactacag ggaccaggga tgatgcaaca tccttgtctt tttatgacag gatgtttgct 300
cagcttctcc aacaataaaa agcacgtggt aaaacacttg cggatattct ggactgtttt 360
taaaaaatat acagtttacc gaaaatcata ttatcttaca atgaaaagga ntttatagat 420
cagccagtga acaacctttt cccaccatac aaaaattcct tttcccgaan gaaaanggct 480
ttctcaataa ncctcacttt cttaanatct tacaagatag ccccganac ttatcgaaac 540
tcattttagg caaatatgan ttttattgtn cgttacttgt ttcaaaattt ggtattgtga 600
atatcaatta ccaccccat ctccatgaa anaaanggga aanggtgaan ttcntaancg 660
cttaaa 666

<210> 77
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 31, 54, 125, 128, 136, 163, 168, 198
<223> n = A,T,C or G

<400> 77
ctgcagcccg ggggatccac taatctacca nggttatattg gcagctaatt ctanatttgg 60

```

atcattgccc aaagttgcac ttgctggtct cttgggattt ggccttgaa aggtatcata 120
catanganta tgccanaata aattccattt ttttgaaaat canctcctg gggctgggtt 180
tggtccacag cataacangc actgcctcct tacctgtgag gaatgcaaaa taaagcatgg 240
attaagtgag aagggagact ctcagccttc agcttcctaa attctgtgtc tgtgactttc 300
gaagtttttt aaacctctga atttgtacac atttaaaatt tcaagtgtac tttaaaataa 360
aatacttcta atgggaacaa aaaaaaaaaa aaaaaa

```

396

<210> 78

<211> 793

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 309, 492, 563, 657, 660, 703, 708, 710, 711, 732, 740, 748, 758, 762, 765, 787

<223> n = A,T,C or G

<400> 78

```

gcatcctagc cgccgactca cacaaggcag gtgggtgagg aaatccagag ttgccatgga 60
gaaaattcca gtgtcagcat tcttgctcct tgtggccctc tcctacactc tggccagaga 120
taccacagtc aaacctggag ccaaaaagga cacaaggac tctcgaccca aactgcccc 180
gacctctcc agaggttggg gtgaccaact catctggact cagacatatg aagaagctct 240
atataaatcc aagacaagca acaaaccctt gatgattatt catcacttgg atgagtgtcc 300
acacagtcna gctttaaaga aagtgtttgc tgaaaataaa gaaatccaga aattggcaga 360
gcagtttgtc ctctcaatc tggtttatga aacaactgac aaacaccttt ctctgatgg 420
ccagtatgtc ccaggattat gtttgttgac ccactctga cagttgaagc cgatatcctg 480
ggaagatatt cnaaccgtct ctatgcttac aaactgcaga tacgctctgt tgcttgacac 540
atgaaaaagc tctcaagttg ctnaaaatga attgtaagaa aaaaaatctc cagccttctg 600
tctgtcggct tgaaaattga aaccagaaaa atgtgaaaaa tggctattgt ggaacanatn 660
gacacctgat taggttttgg ttatgttcac cactattttt aanaaaanan nttttaaat 720
ttggttcaat tntctttttt aaacaatntg tttctacntt gnganctgat ttctaaaaaa 780
aataatnttt ggc

```

793

<210> 79

<211> 456

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 89, 195, 255, 263, 266, 286, 353, 384, 423, 425, 436, 441

<223> n = A,T,C or G

<400> 79

```

actagtatgg ggtgggaggc cccacccttc tcccctaggg gctgttcttg ctccaaaggg 60
ctccgtggag agggactggc agagctgang ccacctgggg ctggggatcc cactcttctt 120
gcagctgttg agcgcaccta accactggtc atgccccac ccctgtcttc cgcaccgcgt 180
tcctcccgac cccangacca ggctacttct cccctcctct tgccctcctc ctgccccctg 240
tgctctgat cgtangaatt gangantgtc ccgccttgtg gctganaatg gacagtggca 300
ggggctggaa atgggtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcnccccccc 360
tgcaagaccg agattgaggg aaancatgtc tgctgggtgt gaccatgttt cctctccata 420
aantnccct gtgacnctca naaaaaaaaa aaaaaa

```

456

<210> 80

<211> 284

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> 283
<223> n = A,T,C or G

<400> 80
ctttgtacct ctagaaaaga taggtattgt gtcatagaaac ttgagtttaa attttatata 60
taaaactaaa agtaatgctc acttttagcaa cacatactaa aattggaacc atactgagaa 120
gaatagcatg acctccgtgc aaacaggaca agcaaatttg tgatgtgttg attaaaaaga 180
aataaataaa tgtgtatatg tgtaacttgt atgtttatgt ggaatacaga ttgggaaata 240
aatgtattt cttactgtga aaaaaaaaaa aaaaaaaaaa aana 284

<210> 81
<211> 671
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 388, 505, 600, 603, 615, 642, 644, 660
<223> n = A,T,C or G

<400> 81
gccaccaaca ttccaagcta ccttgggtac ctttgtgcag tagaagctag tgagcatgtg 60
agcaagcggg gtgcacacgg agactcatcg ttataattta ctatctgcca agagtagaaa 120
gaaaggctgg ggatatttgg gttggcttgg ttttgatttt ttgcttgttt gtttgttttg 180
tactaaaaca gtattatctt ttgaatatcg tagggacata agtatataca tgttatccaa 240
tcaagatggc tagaatggtg cttttctgag tgtctaaaac ttgacacccc tggtaaactc 300
ttcaacacac ttccactgcc tgcgtaatga agttttgatt catttttaac cactggaatt 360
tttcaatgcc gtcattttca gttagatnat tttgcacttt gagattaaaa tgccatgtct 420
atttgattag tcttattttt ttatttttac aggcttatca gtctcactgt tggctgtcat 480
tgtgacaaag tcaaataaac ccccnaggac aacacacagt atgggatcac atattgtttg 540
acattaagct ttggccaaaa aatgttgcag gtgttttacc tcgacttgct aaatcaatan 600
canaaaggct ggctnataat gttggtggtg aaataattaa tnantaacca aaaaaaaaaa 660
aaaaaaaaa a 671

<210> 82
<211> 217
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 35
<223> n = A,T,C or G

<400> 82
ctgcagatgt ttcttgaatg ctttgtcaaa ttaanaaagt taaagtgcaa taatgtttga 60
agacaataag tgggtgtgta tcttgtttct aataagataa acttttttgt ctttgcttta 120
tcttattagg gagttgtatg tcagtgataa aaacatactg tgtggtataa caggcttaat 180
aaattcttta aaaggaaaaa aaaaaaaaaa aaaaaaa 217

<210> 83
<211> 460
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 104, 118, 172, 401, 422, 423, 444, 449
<223> n = A,T,C or G

<400> 83
cgcgagtggg agcaccagga tctcgggctc ggaacgagac tgcacggatt gttttaagaa 60
aatggcagac aaaccagaca tgggggaaat cgccagcttc gatnaggcca agctgaanaa 120
aacggagacg caggagaaga acaccctgcc gaccaaagag accattgagc angagaagcg 180
gagtgaatt tcctaagatc ctggaggatt tcctaccccc gtctctctcg agacccagct 240
cgtgatgtgg aggaagagcc acctgcaaga tggacacgag ccacaagctg cactgtgaac 300
ctgggcactc cgcgccgatg ccaccggcct gtgggtctct gaagggaccc cccccaatcg 360
gactgccaaa ttctccggtt tgccccggga tattatacaa nattatttgt atgaataatg 420
annataaaac acacctcgtg gcancaaana aaaaaaaaaa 460

<210> 84
<211> 323
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 70, 138, 178, 197, 228, 242, 244, 287, 311
<223> n = A,T,C or G

<400> 84
tgggtgatct tggctctgtg gagctgctgg gacgggatct aaaagactat tctggaagct 60
gtggtccaan gcattttgct ggcttaacgg gtcccgaac aaaggacacc agctctctaa 120
aattgaagtt tacccganat aacaatcttt tgggcagaga tgcttatttt aacaaacncc 180
gtccctgcgc aacaacnaac aatctctggg aaataccggc catgaacntg ctgtctcaat 240
cnancatctc tctagctgac cgatcatatc gtcccagatt actacanatc ataataattg 300
atttcctgta naaaaaaaaa aaa 323

<210> 85
<211> 771
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 63, 426, 471, 497, 521, 554, 583, 586, 606, 609, 615, 652,
686, 691, 694, 695, 706, 713, 730, 732, 743, 751
<223> n = A,T,C or G

<400> 85
aaactgggta ctcaacactg agcagatctg ttctttgagc taaaaacat gtgctgtacc 60
aanagtttgc tcttggtgct tttgatgtca gtgctgtac tccacctctg cggcgaatca 120
gaagcaagca actttgactg ctgtcttgga tacacagacc gtattcttca tcctaaattt 180
attgtgggct tcacacggca gctggccaat gaaggctgtg acatcaatgc tatcatcttt 240
cacacaaaga aaaagttgtc tgtgtgcgca aatccaaaac agacttgggt gaaatatatt 300
gtgcgtctcc tcagtaaaaa agtcaagaac atgtaaaaac tgtggctttt ctggaatgga 360
attggacata gcccaagaac agaaagaact tgctgggggt ggaggtttca ctgacacatc 420
atgganggtt tagtgcttat cttatttgtg cctcctggac ttgtccaatt natgaagtta 480
atcatattgc atcatanttt gctttgttta acatcacatt naaattaaac tgtattttat 540
gttatttata gctntagggt ttctgtgttt aactttttat acnaantttc cttaaactatt 600
ttggtntant gcaanttaaa aattatattt ggggggggaa taaatatttg antttctgca 660
gccacaagct ttttttaaaa aaccantaca nccnngttaa atggtnngtc ccnaatgggt 720
tttgcttttn antagaaaaa ttnttagaac natttgaaaa aaaaaaaaaa a 771

<210> 86
<211> 628
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 162, 249, 266, 348, 407, 427, 488, 518, 545, 566, 569, 597,
598, 611, 617, 621, 624
<223> n = A,T,C or G

<400> 86
actagtttgc tttaacatttt tgaaaagtat tatttttgtc caagtgccta tcaactaaac 60
cttgtgtag gtaagaatgg aattttattaa gtgaatcagt gtgacccttc ttgtcataag 120
attatcttaa agctgaagcc aaaatgtgct tcaaaagaaa angactttat tggtcattgt 180
agttcataca ttcaaagcat ctgaactgta gtttctatag caagccaatt acatccataa 240
gtggagaang aaatagatta atgtcnaagt atgattgggt gagggagcaa ggttgaagat 300
aatctggggg tgaaattttc tagttttcat tctgtacatt tttagttinga catcagattt 360
gaaatattaa tgtttacctt tcaatgtgtg gtatcagctg gactcantaa caccctttc 420
ttccctnggg gatggggaat ggattattgg aaaatggaaa gaaaaaagta cttaaagcct 480
tcctttcnca gtttctggct cctaccctac tgatttancc agaataagaa aacattttat 540
catctctgc tttattccca ttaatnaant tttgatgaat aaatctgctt ttatgcnnac 600
ccaaggaatt nagtggnttc ntcnttgt 628

<210> 87
<211> 518
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 384, 421, 486
<223> n = A,T,C or G

<400> 87
ttttttattt ttttagaga gtatgtcagc ttttatttat aaatttattg cctgttttat 60
tataacaaca ttatactgtt tatggtttaa tacatatggt tcaaatgta taatacatca 120
agtagtacag ttttaaaatt ttatgcttaa aacaagtttt gtgtaaaaaa tgcagataca 180
ttttacatgg caaatcaatt ttttaagtcct cctaaaaaatt gatttttttt tgaaatttaa 240
aaacacattt aatttcaatt tctctcttat ataaccttta ttactatagc atgggtttcca 300
ctacagttaa acaatgcagc aaaattccca ttacacggtt aattgggttt taagcggcaa 360
ggttaaaatg ctttgaggat cctnaatacc ctttgaactt caaatgaagg ttatgggtgt 420
naattttaacc ctcatgccat aagcagaagc acaagtttag ctgcattttg ctctaaactg 480
taaaancgag cccccgttg aaaaagcaaa aggggaccc 518

<210> 88
<211> 1844
<212> DNA
<213> Homo sapiens

<400> 88
gagacagtga atcctagtag caaaggattt ttggcctcag aaaaagttgt tgattatttt 60
tattttattt tatttttcga gactccgtct caaaaaaaaa aaaaaaaaaa agaatcacia 120
ggtatttgct aaagcatttt gagctgcttg gaaaaaggga agtagttgca gtagagtttc 180
ttccatcttc ttggtgctgg gaagccatat atgtgtcttt tactcaagct aaggggtata 240
agcttatgtg ttgaatttgc tacatctata ttccacatat tctcacaata agagaatttt 300
gaaatagaaa tatcatagaa catttaagaa agtttagtat aaataatatt ttgtgtgttt 360

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taatcccttt gaagggatct atccaaagaa aatattttac actgagctcc ttcctacacg 420
tctcagtaac agatcctgtg ttagtctttg aaaatagctc atttttttaa tgtcagtgag 480
tagatgtagc atacatatga tgtataatga cgtgtattat gttacaatg tctgcagatt 540
ttgtaggaat acaaaacatg gcctttttta taagcaaaac gggccaatga ctagaataac 600
acatagggca atctgtgaat atgtattata agcagcattc cagaaaagta gttggtgaaa 660
taattttcaa gtcaaaaagg gatatggaaa ggggaattatg agtaacctct attttttaag 720
ccttgctttt aaattaaacg ctacagccat ttaagccttg aggataataa agcttgagag 780
taataatggt aggttagcaa aggttttagat gtatcacttc atgcatgcta ccatgatagt 840
aatgcagctc ttcgagtcac ttctgggtcat tcaagatatt cacccttttg cccatagaaa 900
gcaccctacc tcacctgctt actgacattg tcttagctga tcacaagatc attatcagcc 960
tccattattc cttactgtat ataaaataca gagttttata ttttcctttc ttcgtttttc 1020
accatattca aaacctaaat ttgtttttgc agatggaaatg caaagtaatc aagtgttcgt 1080
gctttcacct agaagggtgt ggtcctgaag gaaagaggtc cctaaatc cccaccctg 1140
gggtgctctc cttccctggt accctgacta ccagaagtca ggtgctagag cagctggaga 1200
agtgcagcag cctgtgcttc cacagatggg ggtgctgctg caacaaggct ttcaatgtgc 1260
ccatcttagg gggagaagct agatcctgtg cagcagcctg gtaagtcctg aggaggttcc 1320
attgctcttc ctgctgctgt cctttgcttc tcaacggggc tcgctctaca gtctagagca 1380
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attgaagtt caaagggtgta ttcaggatcc tcaaagcatt ttaaccttgc cgcttaaaac 1500
ccaatttacc gtgaaatggg aatttttctg cattgttaaa ctgtagtgga aaccatgcta 1560
tagtaataaa ggttatataa gagagaaatt gaaattaaat gtgtttttta atttcaaaaa 1620
aaaatcaatc tttagatga cttaaaaatt gatttgccat gtaaaatgta tctgcatttt 1680
ttacacaaaa cttgttttaa gcataaaaatt ttaaaactgt actacttgat gtattataca 1740
ttttgaacca tatgtattaa accataaaca gtataatgtt gttataataa aacaggcaat 1800
aaatttataa ataaaagctg aaaaaaaaaa aaaaaaaaaa aaaa
1844

```

<210> 89

<211> 523

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 288, 352, 369, 398, 475, 511, 513

<223> n = A,T,C or G

<400> 89

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tttttttttt ttttttttagt caatccacat ttattgatca cttattatgt accaggcact 60
gggataaaga tgactgttag tcaactcacag taaggaagaa aactagcaaa taagacgatt 120
acaatatgat gtagaaaatg ctaagccaga gatatagaaa ggtcctattg ggtccttctg 180
tcaccttgct tttccacatc cctacccttc acaggccttc cctccagctt cctgcccccg 240
ctccccactg cagatcccct gggattttgc ctgagctaa acgagganat gggccccctg 300
gccctggcat gacttgaacc caaccacaga ctgggaaagg gagcctttcg anagtggatc 360
actttgatna gaaaacacat aggggaattga agagaaantc cccaaatggc caccgtgct 420
ggtgctcaag aaaagtttgc agaattggata aatgaaggat caagggaatt aatanatgaa 480
taattgaatg gtggctcaat aagaatgact ncnttgaatg acc
523

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<210> 90

<211> 604

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 563

<223> n = A,T,C or G

<400> 90


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ccagtgtggt ggaatgcaaa gattaccccg gaagctttcg agaagctggg attccctgca 60
gcaaaggaaa tagccaatat gtgtcgtttc tatgaaatga agccagaccg agatgtcaat 120
ctcaccacc aactaaatcc caaagtcaaa agcttcagcc agtttatctc agagaaccag 180
gggagccttc aagggcattg agaaaatcag ctgttcagat aggcctctgc accacacagc 240
ctctttcctc tctgatcctt ttctcttta cggcacaaca ttcatgtttg acagaacatg 300
ctggaatgca attgtttgca acaccgaagg atttcctgcg gtgcctctt cagtaggaag 360
cactgcattg gtgataggac acggtaatgt gattcacatt taacttgcta gttagtata 420
aggggtgta cacctgtttg gtaaaatgag aagcctcgga aacttgggag cttctctcct 480
accactaatg gggagggcag attattactg ggatttctcc tggggtgaat taatttcaag 540
ccctaattgc tgaaattccc ctnggcagcg tccagtttcc tcaactgcat tgcaaaattc 600
cccc 604

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<210> 91
 <211> 858
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 570, 591, 655, 664, 667, 683, 711, 759, 760, 765, 777, 787,
 792, 794, 801, 804, 809, 817, 820
 <223> n = A,T,C or G

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<400> 91
tttttttttt ttttttttta tgattattat tttttttatt gatctttaca tcctcagtgt 60
tggcagagtt tctgatgctt aataaacatt tgttctgatc agataagtgg aaaaaattgt 120
catttcctta ttcaagccat gcttttctgt gatattctga tcctagttga acatacagaa 180
ataaatgtct aaaacagcac ctcgattctc gtctataaca ggactaagtt cactgtgatc 240
ttaaataagc ttggctaataa tgggacatga gtggaggtag tcacacttca gcgaagaaag 300
agaatctcct gtataatctc accaggagat tcaacgaatt ccaccacact ggactagtgg 360
atccccgggg ctgcaggaat tccgatataa gcttatcgat accgtcgacc tcgagggggg 420
gcccgggtacc caattcgccc tatagttagt cgtattacgc gcgctcactg gccgtcgttt 480
tacaacgtcg tgactgggaa aaccctggcg ttaccaact taatcgctt gcagcacatc 540
cccctttcgc cagctggcgt aatagcgaan agcccgcacc gatcgccctt ncaacagtgt 600
cgcagcctga atggcgaatg ggacgcgccc tgtagcggcg cattaaagcg cggcnggggtg 660
tggngnntcc cccacgtgac cgntacactt ggcagcgctc tacgccggtc ntctcgtttc 720
ttcccttctt ttctcgacc gtctgcggg tttcccgann agctnttaat cgggggnctc 780
cctttanggg tncnaattaa nggnttacng gaccttngan cccaaaaact ttgattaggg 840
ggaaggtccc cgaagggg 858

```

<210> 92
 <211> 585
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 317, 319, 320, 321, 325, 327, 328, 330, 331, 332, 460, 462,
 483, 485, 487, 523, 538, 566, 584
 <223> n = A,T,C or G

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<400> 92
gttgaatctc ctggtgagat tatacaggag attctctttc ttcgctgaag tgtgactacc 60
tccactcatg tcccatttta gccaaagctta ttttaagatca cagtgaactt agtcctgtta 120
tagacgagaa tcgagggtgct gtttttagaca tttatttctg tatgttcaac taggatcaga 180
atatcacaga aaagcatggc ttgaataagg aaatgacaat tttttccact tatctgatca 240
gaacaaatgt ttattaagca tcagaaactc tgccaacact gaggatgtaa agatcaataa 300
aaaaaataat aatcatnann naaanannan nngaagggcg gccgccaccg cgggtgagct 360

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ccagcttttg ttcccttttag tgagggttaa ttgcgcgctt ggcgttaatc atgggtcatag 420
 ctgtttcctg tgtgaaattg ttatccggct cacaattccn cncaacatac gagccgggaa 480
 gcntnangtg taaaagcctg ggggtgccta attgagttag ctnactcaca ttaattgngt 540
 tgcgctccac ttgcccgtt ttccantccg ggaaacctgt tcgnc 585

<210> 93

<211> 567

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 82, 158, 230, 232, 253, 266, 267, 268, 269, 270, 271, 272,
 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284,
 285, 286, 287, 295, 303, 307, 314, 349, 352, 354, 356, 366,
 369, 379, 382, 386, 393, 404, 427, 428, 446, 450, 452

<223> n = A,T,C or G

<221> misc_feature

<222> 453, 454, 459, 462, 480, 481, 483, 488, 493, 501, 509, 511,
 512, 518, 520, 525, 526, 532, 541, 557

<223> n = A,T,C or G

<400> 93

cggcagtgtt gctgtctgcg tgtccacctt ggaatctggc tgaactggct gggaggacca 60
 agactgcggc tggggtgggc anggaaggga accgggggct gctgtgaagg atcttggaac 120
 ttccctgtac ccaccttccc ctgtcttcat gtttgtanag gaaccttgtg ccggccaagc 180
 ccagtttctt tgtgtgatac actaatgtat ttgctttttt tgggaaatan anaaaaatca 240
 attaaattgc tantgtttct ttgaannnnn nnnnnnnnnn nnnnnnnngg ggggncgccc 300
 ccncgngnga aacnccccct tttgttccct ttaattgaaa ggttaattng cncnctggc 360
 gttaanccnt gggccaaanc tngttncceg tngtgaaatt gttnatcccc tcccaaattc 420
 cccccnncc ttccaaaccc ggaaancctn annntgttna ancccgggg gttgcctaan 480
 ngnaattnaa ccnaaccccc nttaaattng nntttgcncn ccacnngccc ccttttccca 540
 ntgcggggaa aacctntcc gtgccc 567

<210> 94

<211> 620

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 169, 171, 222, 472, 528, 559, 599

<223> n = A,T,C or G

<400> 94

actagtcaaa aatgctaaaa taatttgga gaaaatattt ttaagtagt gttatagttt 60
 catgtttatc ttttattatg ttttgtgaag ttgtgtcttt tcactaatta cctatactat 120
 gccaatattt ccttatatct atccataaca tttatactac atttgtaana naatatgcac 180
 gtgaaactta acactttata aggtaaaaat gaggtttcca anatttaata atctgatcaa 240
 gttcttgtaa ttccaaata gaatggactt ggtctgttaa gggctaagga gaagagggaag 300
 ataagggtta aagttgttaa tgaccaaaca ttctaaaaga aatgcaaaaa aaaagttat 360
 tttcaagcct tcgaactatt taaggaaagc aaaatcattt cctaaatgca tatcatttgt 420
 gagaatttct cattaatatc ctgaatcatt catttcacta aggtcatgt tnactccgat 480
 atgtctctaa gaaagtacta tttcatggtc caaacctggt tgccatantt gggtaaaggc 540
 tttcccttaa gtgtgaaant atttaaaatg aaattttcct ctttttaaaa attctttana 600
 aggggttaagg gtgttgggga 620

<210> 95
<211> 470
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 61, 67, 79, 89, 106, 213, 271, 281, 330, 354, 387, 432, 448
<223> n = A,T,C or G

<400> 95
ctcgaccttc tctgcacagc ggatgaaccc tgagcagctg aagaccagaa aagccactat 60
nactttntgc ttaattcang agcttacang attcttcaaa gagtngtcc agcatccttt 120
gaaacatgag ttcttaccag cagaagcaga cctttacccc accacctcag cttcaacagc 180
agcaggtgaa acaacccatc cagcctccac ctnaggaaat atttggtccc acaaccaagg 240
agccatgccca ctcaaaggtt ccacaacctg naaacacaaa nattccagag ccaggctgta 300
ccaaggtccc tgagccaggg ctgtaccaan gtccctgagc caggttgtac caangtcctt 360
gagccaggat gtaccaaggt ccctgancca gggtgtccaa ggtccctgag ccaggctaca 420
ccaagggcct gngccaggca gcatcaangt ccctgaccaa ggcttatcaa 470

<210> 96
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 299, 311, 360, 426, 538, 540, 542, 553, 563, 565, 592, 603,
604, 618, 633, 647, 649, 651, 653
<223> n = A,T,C or G

<400> 96
tttttttttt tttttttttt ggaattaaaa gcaatttaat gagggcagag caggaaacat 60
gcatttcttt tcattcgaat cttcagatga accctgagca gccgaagacc agaaaagcca 120
tgaagacttt ctgcttaatt caggggctta caggattctt cagagtgtgt gtgaacaaaa 180
gctttatagt acgtattttt aggatacaaa taagagagag actatggctt ggggtgagaa 240
tgtactgatt acaaggtcta cagacaatta agacacagaa acagatggga agagggtgnc 300
cagcatctgg nggttggtt ctcaagggtt tgtctgtgca ccaaattact tctgcttggn 360
cttctgctga gctgggctg gagtgaccgt tgaaggacat ggctctggta cctttgtgta 420
gcctgncaca ggaactttgg tgtatccttg ctcagggaact ttgatggcac ctggctcagg 480
aaacttgatg aagccttggt caagggacct tgatgcttgc tggctcaggg accttgngn 540
ancctgggct canggacctt tgnncnaacc ttggcttcaa gggacccttg gnacatcctg 600
gcnnaggggac ccttggnncc aaccctgggc ttnagggacc ctttggtntc nanccttggc 660

<210> 97
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 12, 308
<223> n = A,T,C or G

<400> 97
gggaccatac anagtattcc tctcttcaca ccaggaccag ccaactgttgc agcatgagtt 60
cccagcagca gaagcagccc tgcattccac cccctcagct tcagcagcag cagggtgaaac 120

```

agccttgcca gcctccacct caggaacct gcatcccca aaccaaggag cctgccacc 180
ccaaggtgcc tgagccctgc caccccaag tgccctgagcc ctgccagccc aaggttccag 240
agccatgccca cccaagggtg cctgagccct gcccttcaat agtcactcca gcaccagccc 300
agcagaanac caagcagaag taatgtggtc cacagccatg cccttgagga gccggccacc 360
agatgctgaa tcccctatcc cattctgtgt atgagtccca tttgccttgc aattagcatt 420
ctgtctcccc caaaaaaaaa a

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441

<210> 98

<211> 600

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 295, 349, 489, 496, 583

<223> n = A,T,C or G

<400> 98

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gtattctctt cttcacacca ggaccagcca ctgttgagc atgagttccc agcagcagaa 60
gcagccctgc atcccacccc ctcagcttca gcagcagcag gtgaaacagc cttgccagcc 120
tccacctcag gaacctatga tccccaaaac caaggagccc tgccacccc aggtgcctga 180
gccctgccac cccaaagtgc ctgagccctg ccagcccag gttccagagc catgccacc 240
caaggtgcct gagccctgcc cttcaatagt cactccagca ccagcccagc agaanaccaa 300
gcagaagtaa tgtggtccac agccatgccc ttgaggagcc ggccaccana tgctgaatcc 360
cctatcccat tctgtgtatg agtcccattt gccttgcaat tagcattctg tctcccccac 420
aaaagaatgt gctatgaagc tttctttcct acacactctg agtctctgaa tgaagctgaa 480
ggtcttaant acagancatg ttttcagctg ctcagaattc tctgaagaaa agatttaaga 540
tgaaaggcaa atgattcagc tccttattac cccattaaat tcnctttcaa ttccaaaaaa 600

```

<210> 99

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 345, 562, 635

<223> n = A,T,C or G

<400> 99

```

actagtgact gagttcctgg caaagaaatt tgacctggac cagttgataa ctcatgtttt 60
accatttaaa aaaatcagtg aaggatttga gctgctcaat tcaggacaaa gcattcgaac 120
ggtcctgacg ttttgagatc caaagtggca ggaggtctgt gttgtcatgg tgaactggag 180
tttctcttgt gagagttccc tcatctgaaa tcatgtatct gtctcacaaa tacaagcata 240
agtagaagat ttgttgaaaga catagaaccc ttataaagaa ttattaacct ttataaacat 300
ttaaagtcct gtgagcacct gggaattagt ataataacaa tgttnatatt ttgattttac 360
atthttgtaag gctataattg tatcttttaa gaaaacatac cttggatttc tatgtttgaa 420
tgagagatttt taagagtttt aaccagctgc tgcagatata ttactcaaaa cagatatagc 480
gtataaagat atagtaaatg catctcctag agtaatatcc acttaacaca ttggaaacta 540
ttatttttta gatttgaata tnaatgttat tttttaaaca cttgttatga gttacttggg 600
attacatttt gaaatcagtt cattccatga tgcanattac tgggattaga ttaagaaaga 660
cggaaaa

```

667

<210> 100

<211> 583

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> 404, 506, 514, 527, 528, 538, 548, 556, 568, 569
<223> n = A,T,C or G

<400> 100
gttttggttg taagatgatc acagtcattgt tacactgatc taaaggacat atatataacc 60
ctttaaaaaa aaaatcactg cctcattctt atttcaagat gaatttctat acagactaga 120
tgtttttctg aagatcaatt agacattttg aaaatgattt aaagtgtttt ccttaattgt 180
ctctgaaaac aagtttcttt ttagtattta accaaaaaag tgcccttttt gtcactggat 240
tctcctagca ttcattgatt ttttttcata caatgaaatt aaaattgcta aaatcatgga 300
ctggctttct gggtggattt caggtaagat gtgtttaagg ccagagcttt tctcagtatt 360
tgattttttt cccaatattt tgatttttta aaaatataca catnggtgct gcattttatat 420
ctgctggttt aaaattctgt catatttcac ttctagcctt ttagttatgg caaatcatat 480
tttactttta cttaaagcat ttggttattt ggantatctg gttctannct aaaaaaanta 540
attctatnaa ttgaantttt ggtactcnnn catatttgga tcc 583

<210> 101
<211> 592
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 218, 497, 502, 533, 544, 546, 548, 550, 555
<223> n = A,T,C or G

<400> 101
gtggagacgt acaaagagca gccgctcaag acacctggga agaaaaagaa aggcaagccc 60
gggaaacgca aggagcagga aaagaaaaaa cggcgaaact gctctgcctg gtttagactct 120
ggagtgcact ggagtgggct agaaggggac cacctgtctg acacctccac aacgtcgctg 180
gagctcgatt caccgaggca ttgaaatttt cagcaganac cttccaagga catattgcag 240
gattctgtaa tagtgaacat atggaaagta ttagaaatat ttattgtctg taaatactgt 300
aaatgcattg gaataaaaact gtctcccca ttgctctatg aaactgcaca ttggtcattg 360
tgaatatttt tttttttgcc aaggctaata caattattat tatcacattt accataattt 420
attttgtcca ttgatgtatt tattttgtaa atgtatcttg gtgctgctga atttctatat 480
ttttgttaca taatgcnttt anataacct atcaagtttg ttgataaatg acncaatgaa 540
gtgncncnan ttgngggttg aatttaatga atgcctaatt ttattatccc aa 592

<210> 102
<211> 587
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 91, 131, 256, 263, 332, 392, 400, 403, 461, 496, 497, 499,
510, 511, 518, 519, 539, 554, 560, 576
<223> n = A,T,C or G

<400> 102
cgtcctaagc acttagacta catcagggaa gaacacagac cacatccctg tctcatgctg 60
gcttatgttt tctggaagaa agtggagacc nagtccttgg cttaggggct ccccggtggt 120
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ccaggcggat gcccttccc ttagcactac ctggcctcct gcacccctc gcctcatgtt 240
cctcccaact tcaanaaatg aanaaccca tgggcccagc cccttgccct gggaaccaa 300
ggcagccttc caaaactcag gggtgaagc anactattag ggcaggggct gactttgggt 360

gacactgccc attccctctc agggcagctc angtcacccn ggnetcttga acccagcctg 420
 ttcctttgaa aaagggcaaa actgaaaagg gcttttccta naaaaagaaa aaccaggga 480
 ctttgccagg gcttcnmtnt taccaaaacn ncttctcnng gatttttaat tccccattng 540
 gcctccactt accnggggcn atgccccaaa attaanaatt tcccatc 587

<210> 103

<211> 496

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 2, 17, 66, 74, 82, 119, 164, 166, 172, 200, 203, 228, 232,
 271, 273, 415, 423, 445, 446, 473

<223> n = A,T,C or G

<400> 103

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 ctgcanccct tggncactgc anatggaaac ctctcagtgt cttgacatca ccctaccnt 120
 gcggtgggtc tccaccacaa ccactttgac tctgtggtcc ctgnanggtg gnttctcctg 180
 actggcagga tggaccttan ccnacatata cctctgttcc ctctgctnag anaaagaatt 240
 cccttaacat gatataatcc acccatgcaa ntngctactg gccagctac catttaccat 300
 ttgcctacag aatttcatte agtctacact ttggcattct ctctggcgat agagtgtggc 360
 tgggctgacc gcaaaagggtg ccttacacac tggccccac cctcaaccgt tgacncatca 420
 gangcttgcc tcctccttct gattnncccc catgttggat atcagggtgc tcnagggatt 480
 ggaaaagaaa caaaac 496

<210> 104

<211> 575

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 18, 19, 45, 68, 77, 132, 155, 174, 219, 226, 238, 259, 263,
 271, 273, 306, 323, 339, 363, 368, 370, 378, 381, 382, 436,
 440, 449, 450, 456, 481, 485, 496, 503, 510, 512, 515, 528,
 542, 552

<223> n = A,T,C or G

<400> 104

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 ctgttcaact cngtttgtgt ctgggggata aactnggggc tatggaagcg gctnaactgt 180
 tgttttggtg gaagggctgg taattggcct tgggaagtng cttatngaag ttggcctnng 240
 gaagttgcta ttgaaagtng ccntggaagt ngntttgggtg gggggttttg ctggtggcct 300
 ttgttnaatt tgggtgcttt gtnaatggcg gccccctcnc ctgggcaatg aaaaaaatca 360
 ccnatgcngn aaacctcnac nnaacagcct gggcttccct cacctcgaaa aaagttgctc 420
 ccccccaaaa aaaggncaan ccctcaann tggaangttg aaaaaatcct cgaatgggga 480
 nccnnaaaac aaaaancccc cntttcccn gnaanggggg aaataccncc cccccactta 540
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<210> 105

<211> 619

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> 260, 527, 560, 564, 566, 585, 599
<223> n = A,T,C or G

<400> 105
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tgcataaagc caatgtagtc cagtttctaa gatcatgttc caagctaact gaatcccact 180
tcaatacaca ctcatgaact cctgatggaa caataacagg cccaagcctg tggtagatg 240
tgcacacttg ctagactcan aaaaaatact actctcataa atgggtggga gtattttggt 300
gacaacctac tttgcttggc tgagtgaagg aatgatattc atatattcat ttattccatg 360
gacatttagt tagtgctttt tatataccag gcatgatgct gagtgacact cttgtgtata 420
tttccaaatt tttgtacagt cgctgcacat atttgaaatc atatattaag acttccaaaa 480
aatgaagtcc ctgggttttc atggcaactt gatcagtaaa ggattcncct ctgtttggtg 540
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aagtgggtggg gaaaaaaaaa 619

<210> 106
<211> 506
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 8, 21, 31, 32, 58, 75, 89, 96, 99, 103, 122, 126, 147, 150,
158, 195, 210, 212, 219, 226, 246, 248, 249, 255, 258, 261,
263, 265, 275, 304, 317, 321, 331, 337, 340, 358, 371, 377,
380, 396, 450, 491
<223> n = A,T,C or G

<400> 106
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angtanagat gttctggata ccattanatn tgccccngt gtcagaggct catattgtgt 180
tatgtaaatg gtatntcatt cgctactatn antcaattng aaatanggtc tttgggttat 240
gaatanntng cagcncanct nanangctgt ctgtngtatt cattgtggtc atagcacctc 300
acancattgt aacctcnatc nagtgagaca nactagnaan ttccatagtg tggtcanga 360
ttccaaatgg nctcatntcn aatgttttaa agttanttaa gtgtaagaaa tacagactgg 420
atgttccacc aactagtacc tgtaatgacn ggccctgtccc aacacatctc ccttttccat 480
gactgtggtgta ncccgcatcg gaaaaa 506

<210> 107
<211> 452
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 289, 317, 378
<223> n = A,T,C or G

<400> 107
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tttaaagacc ctctattct ataaaactct gcatgtagag gcttgtttac ctttctctct 180
ctaaggttta caataggagt ggtgatttga aaaatataaa attatgagat tgggttttct 240
gtggcataaa ttgcatcact gtatcatttt cttttttaac cggtgaagant ttcagtttgt 300
tggaagtaaa ctgtganaac ccagtttccc gtccatctcc cttagggact acccatagaa 360

catgaaaagg tccccacnga agcaagaaga taagtctttc atggctgctg gttgcttaaa 420
ccacttttaa accaaaaaat tccccttgga aa 452

<210> 108

<211> 502

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 22, 31, 126, 168, 183, 205, 219, 231, 236, 259, 283, 295,
296, 298, 301, 340, 354, 378, 383, 409, 433, 446, 455, 466,
488

<223> n = A,T,C or G

<400> 108

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agaccncaac tgaagcttaa aaaatctatc acatgtataa tacctttnga agaacattaa 180
tanagcatat aaaactttta acatntgctt aatgttgtnc aattataaaa ntaatngaaa 240
aaaatgtccc tttaacatnc aatatcccac atagtgttat ttnaggggat taccnngnaa 300
naaaaaaagg gtagaaggga tttaatgaaa actctgcttn ccatttctgt ttanaaacgt 360
ctccagaaca aaaacttntc aantctttca gctaaccgca tttgagctna ggccactcaa 420
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accctggnta ctctgcct ca 502

<210> 109

<211> 1308

<212> DNA

<213> Homo sapiens

<400> 109

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ggcatcttga ctgcaattgg catggtcttc ctggggaccc gaggagccac cgcttcccag 180
ttggaggagg tgtttcactc tgaaaagag acgaagagct caagaataaa ggctgaagaa 240
aaagagggtga ttgagaacac agaagcagta catcaacaat tccaaaagtt ttgactgaa 300
ataagcaaac tcactaatga ttatgaactg aacataacca acaggctgtt tggagaaaaa 360
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gaacctgttg attttgtaaa tgcagccgat gaaagtcgaa agaagattaa ttcttgggtt 480
gaaagcaaaa caaatgaaaa aatcaaggac ttgttcccag atggctctat tagtagctct 540
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gatgatcgtt gccatggcat tgctgctttt agcaaaaaac aactaccagt gttactcata 1260
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<210> 110

<211> 391

<212> PRT

<213> Homo sapiens

<400> 110

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          20          25          30
Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
          35          40          45
Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
          50          55          60
Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Ile Glu Asn Thr Glu
65          70          75          80
Ala Val His Gln Gln Phe Gln Lys Phe Leu Thr Glu Ile Ser Lys Leu
          85          90          95
Thr Asn Asp Tyr Glu Leu Asn Ile Thr Asn Arg Leu Phe Gly Glu Lys
          100          105          110
Thr Tyr Leu Phe Leu Gln Lys Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr
          115          120          125
His Ala Ser Leu Glu Pro Val Asp Phe Val Asn Ala Ala Asp Glu Ser
130          135          140
Arg Lys Lys Ile Asn Ser Trp Val Glu Ser Lys Thr Asn Glu Lys Ile
145          150          155          160
Lys Asp Leu Phe Pro Asp Gly Ser Ile Ser Ser Ser Thr Lys Leu Val
          165          170          175
Leu Val Asn Met Val Tyr Phe Lys Gly Gln Trp Asp Arg Glu Phe Lys
          180          185          190
Lys Glu Asn Thr Lys Glu Glu Lys Phe Trp Met Asn Lys Ser Thr Ser
          195          200          205
Lys Ser Val Gln Met Met Thr Gln Ser His Ser Phe Ser Phe Thr Phe
210          215          220
Leu Glu Asp Leu Gln Ala Lys Ile Leu Gly Ile Pro Tyr Lys Asn Asn
225          230          235          240
Asp Leu Ser Met Phe Val Leu Leu Pro Asn Asp Ile Asp Gly Leu Glu
          245          250          255
Lys Ile Ile Asp Lys Ile Ser Pro Glu Lys Leu Val Glu Trp Thr Ser
          260          265          270
Pro Gly His Met Glu Glu Arg Lys Val Asn Leu His Leu Pro Arg Phe
          275          280          285
Glu Val Glu Asp Ser Tyr Asp Leu Glu Ala Val Leu Ala Ala Met Gly
290          295          300
Met Gly Asp Ala Phe Ser Glu His Lys Ala Asp Tyr Ser Gly Met Ser
305          310          315          320
Ser Gly Ser Gly Leu Tyr Ala Gln Lys Phe Leu His Ser Ser Phe Val
          325          330          335
Ala Val Thr Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Gly Ile Gly
          340          345          350
Phe Thr Val Thr Ser Ala Pro Gly His Glu Asn Val His Cys Asn His
          355          360          365
Pro Phe Leu Phe Phe Ile Arg His Asn Glu Ser Asn Ser Ile Leu Phe
          370          375          380
Phe Gly Arg Phe Ser Ser Pro
385          390

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<210> 111

<211> 1419

<212> DNA

<213> Homo sapiens

<400> 111

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ggcaacatct tcttttcccc tgtgggcac ttgactgcaa ttggcatggg cctcctgggg 240
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attgagaaca cagaagcagt acatcaacaa ttccaaaagt ttttgactga aataagcaaa 420
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1419

<210> 112

<211> 400

<212> PRT

<213> Homo sapiens

<400> 112

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Met Asp Ser Leu Gly Ala Val Ser Thr Arg Leu Gly Phe Asp Leu Phe
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Lys Glu Leu Lys Lys Thr Asn Asp Gly Asn Ile Phe Phe Ser Pro Val
20      25      30
Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
35      40      45
Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
50      55      60
Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Val Arg Ile Lys Ala
65      70      75      80
Glu Gly Lys Glu Ile Glu Asn Thr Glu Ala Val His Gln Gln Phe Gln
85      90      95
Lys Phe Leu Thr Glu Ile Ser Lys Leu Thr Asn Asp Tyr Glu Leu Asn
100      105      110
Ile Thr Asn Arg Leu Phe Gly Glu Lys Thr Tyr Leu Phe Leu Gln Lys
115      120      125
Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr His Ala Ser Leu Glu Pro Val
130      135      140
Asp Phe Val Asn Ala Ala Asp Glu Ser Arg Lys Lys Ile Asn Ser Trp
145      150      155      160
Val Glu Ser Lys Thr Asn Glu Lys Ile Lys Asp Leu Phe Pro Asp Gly
165      170      175
Ser Ile Ser Ser Thr Lys Leu Val Leu Val Asn Met Val Tyr Phe
180      185      190

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Lys Gly Gln Trp Asp Arg Glu Phe Lys Lys Glu Asn Thr Lys Glu Glu
 195 200 205
 Lys Phe Trp Met Asn Lys Ser Thr Ser Lys Ser Val Gln Met Met Thr
 210 215 220
 Gln Ser His Ser Phe Ser Phe Thr Phe Leu Glu Asp Leu Gln Ala Lys
 225 230 235 240
 Ile Leu Gly Ile Pro Tyr Lys Asn Asn Asp Leu Ser Met Phe Val Leu
 245 250 255
 Leu Pro Asn Asp Ile Asp Gly Leu Glu Lys Ile Ile Asp Lys Ile Ser
 260 265 270
 Pro Glu Lys Leu Val Glu Trp Thr Ser Pro Gly His Met Glu Glu Arg
 275 280 285
 Lys Val Asn Leu His Leu Pro Arg Phe Glu Val Glu Asp Ser Tyr Asp
 290 295 300
 Leu Glu Ala Val Leu Ala Ala Met Gly Met Gly Asp Ala Phe Ser Glu
 305 310 315 320
 His Lys Ala Asp Tyr Ser Gly Met Ser Ser Gly Ser Gly Leu Tyr Ala
 325 330 335
 Gln Lys Phe Leu His Ser Ser Phe Val Ala Val Thr Glu Glu Gly Thr
 340 345 350
 Glu Ala Ala Ala Ala Thr Gly Ile Gly Phe Thr Val Thr Ser Ala Pro
 355 360 365
 Gly His Glu Asn Val His Cys Asn His Pro Phe Leu Phe Phe Ile Arg
 370 375 380
 His Asn Glu Ser Asn Ser Ile Leu Phe Phe Gly Arg Phe Ser Ser Pro
 385 390 395 400

<210> 113

<211> 957

<212> DNA

<213> Homo sapiens

<400> 113

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<210> 114

<211> 161

<212> PRT

<213> Homo sapiens

<400> 114

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<220>
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<222> 8, 21, 31, 32, 58, 75, 89, 96, 99, 103, 122, 126, 147, 150,
158, 195, 210, 212, 219, 226, 246, 248, 249, 255, 258, 261,
263, 265, 275, 304, 317, 321, 331, 337, 340, 358, 371, 377,
380, 396, 450, 491
<223> n = A,T,C or G
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<210> 116
<211> 3079
<212> DNA
<213> Homo sapiens
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```

```

<210> 120
<211> 587
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc feature
<222> 91, 131, 256, 263, 332, 392, 400, 403, 461, 496, 497, 499,
510, 511, 518, 519, 539, 554, 560, 576
<223> n = A,T,C or G

```

```

<400> 120
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ccaggcggat gccccttccc ttagcactac ctggcctcct gcacccctc gcctcatgtt 240
cctcccacct tcaanaaatg aanaaccca tgggccagc cccttgccct gggaaccaa 300
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```

```

<210> 121
<211> 619
<212> DNA
<213> Homo sapiens

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<220>
<221> misc feature
<222> 260, 527, 560, 564, 566, 585, 599
<223> n = A,T,C or G

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<400> 121
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tgcacacttg ctgactcan aaaaaatact actctcataa atgggtggga gtattttggt 300
gacaacctac tttgcttggc tgagtgaagg aatgatattc atatattcat ttattccatg 360
gacatttagt tagtgctttt tatataccag gcatgatgct gagtgacact cttgtgtata 420
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```

```

<210> 122
<211> 1475
<212> DNA
<213> Homo sapiens

```

<400> 122

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```

1475

<210> 123

<211> 2294

<212> DNA

<213> Homo sapiens

<400> 123

```

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tgatttttct gatg 2294

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<210> 124

<211> 956

<212> DNA

<213> Homo sapiens

<400> 124

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cagattgaga acctcaagga ggagctggcc tacctgaaga agaaccacga ggaggagatg 180
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```

<210> 125

<211> 486

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 16

<223> n = A,T,C or G

<400> 125

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tttact 486

```

<210> 126
<211> 3552
<212> DNA
<213> Homo sapiens

<400> 126
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<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 546

<212> DNA

<213> Homo sapiens

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<211> 5156

<212> DNA

<213> Homo sapiens

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<211> 671

<212> DNA

<213> Homo sapiens

<400> 131

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671

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<211> 590
<212> DNA
<213> Homo sapiens

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<211> 581
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<212> DNA
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<210> 135

<211> 2856

<212> DNA

<213> Homo sapiens

<400> 135

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 cgacgcgccg tcgccaccog cgtaccoggc gcagccagag ccaccagcgc agcgctgcca 180
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atatctggac aagccaactt gtaaatacac cacctcactc ctgttactta cctaaacaga 2520
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tttgatccct gttacccaga gaatatatac attctttatc ttgacattca aggcatttct 2760
atcacatatt tgatagttgg tgttcaaaaa aacactagtt ttgtgccagc cgtgatgctc 2820
aggcttgaaa tcgcattatt ttgaatgtga agggaa 2856

```

<210> 136
 <211> 356
 <212> DNA
 <213> Homo sapiens

```

<400> 136
ggtggagcca aatgaagaaa atgaagatga aagagacaga cacctcagtt tttctggatc 60
aggcattgat gatgatgaag attttatctc cagcaccatt tcaaccacac caggggcttt 120
tgaccacaca aaacagaacc aggactggac tcagtgaac ccaagccatt caaatccgga 180
agtgtacttt cagacaacca caaggatgac tgatgtagac agaaatggca ccactgctta 240
tgaaggaaac tggaaccag aagcacaccc tccctcatt caccatgagc atcatgagga 300
agaagagacc ccacattcta caagcacaat ccaggcaact cctagtagta caacgg 356

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<210> 137
 <211> 356
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 254, 264, 279, 281, 290, 328, 342
 <223> n = A,T,C or G

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<400> 137
gcagggtggag aagacatttt attgttcctg gggctctctg aggccattg gtggggctgg 60
gtcactggct gcccccgaa cagggcgctg ctccatggct ctgcttgtgg tagtctgtgg 120
ctatgtctcc cagcaaggac agaaactcag aaaaatcaat cttcttatcc tcattcttgt 180
cctttttctc aaagacatcg gcgaggtaat ttgtgccctt tttacctcg cccgcgacca 240
cgctaaggcc aaanttcag acanayggcc gggccggtnc nataggggan cccaacttgg 300
ggaccctaac tctggcgcg aaacacangg gcataagctt gnttcctgtg gggaaa 356

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<210> 138
 <211> 353
 <212> DNA
 <213> Homo sapiens

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<400> 138
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aatagacact tagatttctc tcttgtggga agaaaccacc tgtccatcca ctgactcttc 120
tacattgatg tggaaattgc tgctgctacc accacctcct gaagaggctt ccctgatgcc 180
aatgccagcc atcttggcat cctggccctc gagcaggctg cggtaagtag cgatctcctg 240
ctccagccgt gtctttatgt caagcagcat cttgtactcc tggttctgag cctccatctc 300
gcctcgagac tcactcagac ctcgscgsg mssmcgctam gccgaattcc agc 353

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<210> 139
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 139

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agcgtgggtcg cggccgaggt ccatccgaag caagattgca gatggcagtg tgaagagaga 60
agacatattc tacacttcaa agctttgggtg caattcccat cgaccagagt tgggccgacc 120
agccttggaag aggtcactga aaaatcttca attggattat gttgacctct acctattca 180
ttttccagtg tctgtaaaagc caggtgagga agtgatccca aaagatgaaa atggaaaaat 240
actatttgac acagtggatc tctgtgccac gtgggaggcc gtggagaagt gtaaagatgc 300
aggattggac ctgccgggc ggccgctcga aagccgaatt ccagcacact ggcggccgtt 360
actagtggat c

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<210> 140

<211> 370

<212> DNA

<213> Homo sapiens

<400> 140

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tagcgtgggtc gcgcccgagg tccatctccc tttgggaact agggggctgc tgggtggaaa 60
tgggagccag ggcagatggt gcattccttt gtgtccctgt aaatgtggga ctacaagaag 120
aggagctgcc tgagtggtag tttctcttcc tggtaatcct ctggcccagc ctcattggcag 180
aatagaggta tttttaggct atttttgtaa tatggcttct ggtcaaaatc cctgtgtagc 240
tgaattccca agccctgcat tgtacagccc cccactcccc tcaccaccta ataaaggaat 300
agttaacact caaaaaaaaa aaaaaacctg cccgggaggc cgctcgaaag ccgaattcca 360
gcacactggc

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<210> 141

<211> 371

<212> DNA

<213> Homo sapiens

<400> 141

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tagcgtgggtc gcgcccgagg tcctctgtgc tgcctgtcac agcccgatgg taccagcgca 60
gggtgtaggc agtgcaggag ccctcatcca gtggcaggga acaggggtca tcactatccc 120
aaggagcttc aggtcctggt tactcctcca cagaatactc ggagtattca gactactcat 180
catcctcagg ggttaccgac tcttctctct ctgcatgaga gacgcggagc acaggcacag 240
catggagctg ggagccggca gtgtctgcag cataactagg gaggggtcgt gatccagatg 300
cgatgaactg gccttggcag gcacagtgtg gactcatctc ttggcgacct gcccgggcgg 360
ccgctcgaag c

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<210> 142

<211> 343

<212> DNA

<213> Homo sapiens

<400> 142

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gcgttttgag gccaatggtg taaaaggaaa tatcttcaca taaaaactag atggaagcat 60
tgtcagaaac ctctttgtga tgtttgcttt caactcacag agttgaacat tccttttcat 120
agagcagttt tgaacactc tttttagtaa ttgcaagcg gatgattgga tcgctatgag 180
gtcttcattg gaaacgggat acctttacat aaaaactaga cagtagcatt ctcagaaatt 240
tctttgggat gtgggcattc aaccacaga ggagaacttc atttgataga gcagttttga 300
aacacccttt ttgtagaatc tacaggtgga cathtagagt gct

```

<210> 143

<211> 354

<212> DNA

<213> Homo sapiens

<400> 143

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aggtctgatg gcagaaaaac tcagactgtc tgcaacttta cagatgggtg attggttcag 60
catcaggagt gggatgggaa ggaaagcaca ataacaagaa aattgaaaga tgggaaatta 120
gtgggtggagt gtgtcatgaa caatgtcacc tgtactcgga tctatgaaaa agtagaataa 180

```

```

aaattccatc atcacttttg acaggagtta attaagagaa tgaccaagct cagttcaatg 240
agcaaattct catactgttt ctttcttttt tttttcatta ctgtgttcaa ttatctttat 300
cataaacatt ttacatgcag ctatttcaaa gtgtgttgga ttaattagga tcat 354

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<210> 144
<211> 353
<212> DNA
<213> Homo sapiens

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<400> 144
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cctagagcac atctggatct cagccccacc cctggcaacc tgctgccta gagaactccc 120
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gttaagtgtc ttaactttca ttctgtctta cgatagtctt cagaggtggg aacagatgaa 240
gaaaccatgc ccagagagaag gttaagtgtc ttctcttcta tggagccagt gttccaacct 300
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```

```

<210> 145
<211> 371
<212> DNA
<213> Homo sapiens

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<400> 145
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ttcctgagac ttgctggcct ctccgttgag tccacttgcc tttctgtcct ccacagctcc 120
attgccactg ttgatcacta gctttttctt ctgccacac cttcttcgac tgttgactgc 180
aatgcaaact gcaagaatca aagccaaggc caagagggat gccaatga tcagccattc 240
tggaatttgg ggtgtcctta taggaccaga gggtgtgtt gctccacctt cttgactccc 300
atgtgagacc tcggccgcga ccacgctaag ccgaattcca gcacactggc ggcccgttac 360
tagtgatcc g 371

```

```

<210> 146
<211> 355
<212> DNA
<213> Homo sapiens

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<400> 146
ggtcctccgt cctcttccca gaggtgtcgg ggcttggccc cagcctccat cttcgtctct 60
caggatggcg agtagcagcg gctccaaggc tgaattcatt gtcggaggga aatataaact 120
ggtacggaag atcgggtctg gtccttcgg ggacatctat ttggcgatca acatcaccaa 180
cggcgaggaa gtggcagtga agctagaatc tcagaaggcc aggcattccc agttgctgta 240
cgagagcaag ctctataaga ttcttcaagg tggggttggc atccccaca tacggtggta 300
tggtcaggaa aaagactaca atgtactagt catggatctt ctgggacctc gcctc 355

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```

<210> 147
<211> 355
<212> DNA
<213> Homo sapiens

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<400> 147
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tactatgcac gtgctgtgat tttgaacata actcgtccca aaaacttgtc acgatcatcc 120
tgacttttta ggttggctga tccatcaatc ttgcaactca ctgttacttc tttcccagt 180
ttgttaggag caaagctgac ctgaacagca accaatggct gtagataccc aacatgcagt 240
tttttcccat aatatgggaa atattttaag tctatcatc cattatgagg ataaactgct 300
acatttggtg tatcttcatt ctttgaaaca caatctatcc ttggcactcc ttcat 355

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```

<210> 148

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<211> 369
 <212> DNA
 <213> Homo sapiens

<400> 148
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 cacccttctt catgatgtgg gaagagtgtt gcaaccacgc cctagccaac accgcatgag 120
 agggagtgtg ccgagggctt ctgagaaggt ttctctcaca tctagaaaga agcgcttaag 180
 atgtggcagc cctcttctt caagtggctc ttgtcctgtt gccctgggag ttctcaaatt 240
 gctgcagcag cctccatcca gcctgaggat gacatcaata cacagaggaa gaagagtcag 300
 gaaaagatga gagaagttac agactctcct gggcgacccc gagagcttac cattcctcag 360
 acttcttca 369

<210> 149
 <211> 620
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 169, 171, 222, 472, 528, 559, 599
 <223> n = A,T,C or G

<400> 149
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 catgtttatc ttttattatg ttttgtgaag ttgtgtcttt tcactaatta cctatactat 120
 gccaatattt ccttatatct atccataaca ttctactac atttgtaana naatatgcac 180
 gtgaaactta acactttata aggtaaaaat gaggtttcca anatttaata atctgatcaa 240
 gttcttgtta ttccaaata gaatggactt ggtctgttaa gggctaagga gaagaggaag 300
 ataaggttaa aagtgtgtaa tgaccaaaca ttctaaaaga aatgcaaaaa aaaagtattat 360
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 gagaatttct cattaatatc ctgaatcatt catttcaact aggtcatgt tnatccgat 480
 atgtctctaa gaaagtacta tttcatggtc caaacctggt tgccatantt gggtaaaggc 540
 tttcccttaa gtgtgaaant atttaaaatg aaattttcct ctttttaaaa attctttana 600
 aggttaagg gtgttgggga 620

<210> 150
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 150
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 gagcaaccag tatcacttcc ctgtttataa aacctctaac catctctttg ttctttgaac 120
 atgtgaaaa ccacctggtc tgcatgtatg ccgaatttg yaattctttt ctctcaaagt 180
 aaaatttaat tttagggatt catttctata tttcacata ttagtatta ttatttcctt 240
 atatgtgtaa ggtgaaattt atggattttg agtgtgcaag aaaatatatt tttaaagctt 300
 tcatttttcc ccagtgaaat gatttagaat tttttatgta aatatacaga atgttttttc 360
 ttacttttat a 371

<210> 151
 <211> 4655
 <212> DNA
 <213> Homo sapiens

<400> 151
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acatgtttgta	cctggaaaac	aatgccacaga	ctcaatttag	tgagccacag	tacacgaacc	180
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ataacacaga	ccacgcgcag	aacagcgta	cggcgccctc	gccctacgca	cagcccagct	300
ccaccttcga	tgtctctct	ccatcacccg	ccatcccctc	caacaccgac	taccagggcc	360
cgcacagttt	cgacgtgtcc	ttccagcagt	cgagcaccgc	caagtcggcc	acctggacgt	420
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<210> 152

<211> 586

<212> PRT

<213> Homo sapiens

<400> 152

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20     25     30
Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
35     40     45
Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
50     55     60
Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
65     70     75     80
His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
85     90     95
Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
100    105    110
Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Gln Gly
115    120    125
Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
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Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
145    150    155    160
Glu Gly Gln Ile Ala Pro Ser Ser His Leu Ile Arg Val Glu Gly Asn
165    170    175
Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
180    185    190
Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
195    200    205
Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
210    215    220
Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
225    230    235    240
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<210> 153
<211> 2007
<212> DNA
<213> Homo sapiens
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2007

<210> 154

<211> 2148

<212> DNA

<213> Homo sapiens

<400> 154

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<210> 155

<211> 153

<212> PRT

<213> Homo sapiens

<400> 155

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Pro Met Gly Asp Val Pro Met Asp Gly Ile Ser Val Ala Asp Ile Gly
 35           40           45
Ala Ala Val Ser Ser Ile Phe Asn Ser Pro Glu Glu Phe Leu Gly Lys
 50           55           60
Ala Val Gly Leu Ser Ala Glu Ala Leu Thr Ile Gln Gln Tyr Ala Asp
 65           70           75           80
Val Leu Ser Lys Ala Leu Gly Lys Glu Val Arg Asp Ala Lys Ile Thr
 85           90           95
Pro Glu Ala Phe Glu Lys Leu Gly Phe Pro Ala Ala Lys Glu Ile Ala
100           105           110
Asn Met Cys Arg Phe Tyr Glu Met Lys Pro Asp Arg Asp Val Asn Leu
115           120           125
Thr His Gln Leu Asn Pro Lys Val Lys Ser Phe Ser Gln Phe Ile Ser
130           135           140
Glu Asn Gln Gly Ala Phe Lys Gly Met
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<210> 156

<211> 128

<212> PRT

<213> Homo sapiens

<400> 156

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 20           25           30
Pro Met Gly Asp Val Pro Met Asp Gly Ile Ser Val Ala Asp Ile Gly
 35           40           45
Ala Ala Val Ser Ser Ile Phe Asn Ser Pro Glu Glu Phe Leu Gly Lys
 50           55           60
Ala Val Gly Leu Ser Ala Glu Ala Leu Thr Ile Gln Gln Tyr Ala Asp
 65           70           75           80
Val Leu Ser Lys Ala Leu Gly Lys Glu Val Arg Asp Ala Lys Thr Ile
 85           90           95
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<210> 157
 <211> 424
 <212> DNA
 <213> Homo sapiens

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 <221> misc_feature
 <222> 320, 322
 <223> n = A, T, C or G

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 <211> 2099
 <212> DNA
 <213> Homo sapiens

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<210> 159

<211> 291

<212> PRT

<213> Homo sapiens

<400> 159

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			20					25					30		
Val	Met	Ile	Leu	Val	Val	Ala	Ala	Gln	Glu	Val	Trp	Gly	Asp	Glu	Gln
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Leu	Ile	Phe	Val	Ser	Thr	Pro	Ala	Leu	Leu	Val	Ala	Met	His	Val	Ala
				85					90					95	
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Ile	Phe	Met	Ile	Ser	Ala	Ser	Val	Ile	Cys	Met	Leu	Leu	Asn	Val	Ala
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Glu	Leu	Cys	Tyr	Leu	Leu	Leu	Lys	Val	Cys	Phe	Arg	Arg	Ser	Lys	Arg
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					230					235				240	
Gln	Asn	Glu	Met	Asn	Glu	Leu	Ile	Ser	Asp	Ser	Gly	Gln	Asn	Ala	Ile
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Thr	Gly	Ser	Gln	Ala	Lys	His	Phe	Lys	Val	Lys	Cys	Ser	Cys	Val	Ile
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<210> 160

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 160

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<210> 161

<211> 943

<212> PRT

<213> Homo sapiens

<400> 161

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Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met
      50          55          60
Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val
      65          70          75          80
Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Thr Trp Lys Ala Asn
      85          90          95
Asn Asn Ser Lys Ile Lys Gln Glu Ser Tyr Glu Lys Ala Asn Val Ile
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Val Thr Asp Trp Tyr Gly Ala His Gly Asp Asp Pro Tyr Thr Leu Gln
      115          120          125
Tyr Arg Gly Cys Gly Lys Glu Gly Lys Tyr Ile His Phe Thr Pro Asn
      130          135          140
Phe Leu Leu Asn Asp Asn Leu Thr Ala Gly Tyr Gly Ser Arg Gly Arg
      145          150          155          160
Val Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe Asp Glu
      165          170          175
Tyr Asn Asn Asp Lys Pro Phe Tyr Ile Asn Gly Gln Asn Gln Ile Lys
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      275          280          285
Phe Pro Met Asn Gly Thr Glu Leu Pro Pro Pro Pro Thr Phe Ser Leu
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 Ser Asn Asp Asp Arg Lys Leu Leu Val Ser Tyr Leu Pro Thr Thr Val
 370 375 380
 Ser Ala Lys Thr Asp Ile Ser Ile Cys Ser Gly Leu Lys Lys Gly Phe
 385 390 395 400
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 405 410 415
 Leu Val Thr Ser Gly Asp Asp Lys Leu Leu Gly Asn Cys Leu Pro Thr
 420 425 430
 Val Leu Ser Ser Gly Ser Thr Ile His Ser Ile Ala Leu Gly Ser Ser
 435 440 445
 Ala Ala Pro Asn Leu Glu Glu Leu Ser Arg Leu Thr Gly Gly Leu Lys
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 Ser Arg Ile Ser Ser Gly Thr Gly Asp Ile Phe Gln Gln His Ile Gln
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 Leu Glu Ser Thr Gly Glu Asn Val Lys Pro His His Gln Leu Lys Asn
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 Thr Ala Ser Leu Trp Ile Pro Gly Thr Ala Lys Pro Gly His Trp Thr
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 Tyr Thr Leu Asn Asn Thr His His Ser Leu Gln Ala Leu Lys Val Thr
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 Val Thr Ser Arg Ala Ser Asn Ser Ala Val Pro Pro Ala Thr Val Glu
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 675 680 685
 Val His Val Asn His Ser Pro Ile Ser Thr Pro Ala His Ser Ile
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 Pro Gly Ser His Ala Met Tyr Val Pro Gly Tyr Thr Ala Asn Gly Asn
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 Ile Arg Glu Ile Phe Thr Phe Ser Pro Gln Ile Ser Thr Asn Gly Pro
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 Glu His Gln Pro Asn Gly Glu Thr His Glu Ser His Arg Ile Tyr Val
 850 855 860
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 Ala Arg Asp Tyr Leu Ile Leu Lys Gly Val Leu Thr Ala Met Gly Leu
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<211> 498

<212> DNA

<213> Homo sapiens

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<211> 1128

<212> DNA

<213> Homo sapiens

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<211> 1310

<212> DNA

<213> Homo sapiens

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<211> 177

<212> PRT

<213> Homo sapiens

<400> 165

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 Lys Ser Ile Gln Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile
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 65 70 75 80
 Asn Ser Lys Pro Ser Pro Asn Thr Lys Asn His Pro Val Arg Phe Gly
 85 90 95
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 Thr Tyr Lys Glu Gln Pro Leu Lys Thr Pro Gly Lys Lys Lys Gly
 115 120 125
 Lys Pro Gly Lys Arg Lys Glu Glu Lys Lys Lys Arg Arg Thr Arg

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<210> 166
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 65 70 75 80
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 85 90 95
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<210> 167
 <211> 3362
 <212> DNA
 <213> Homo sapiens

<400> 167
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<211> 2784

<212> DNA

<213> Homo sapiens

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<210> 169

<211> 592

<212> PRT

<213> Homo sapiens

<400> 169

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20           25           30
Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn
35           40           45
Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met
50           55           60
Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val

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 85 Asn Asn Ser Lys Ile Lys Gln Glu Ser Tyr Glu Lys Ala Asn Val Ile 95
 100 Val Thr Asp Trp Tyr Gly Ala His Gly Asp Asp Pro Tyr Thr Leu Gln 110
 115 Tyr Arg Gly Cys Gly Lys Glu Gly Lys Tyr Ile His Phe Thr Pro Asn 125
 130 Phe Leu Leu Asn Asp Asn Leu Thr Ala Gly Tyr Gly Ser Arg Gly Arg 140
 145 Val Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe Asp Glu 155
 165 Tyr Asn Asn Asp Lys Pro Phe Tyr Ile Asn Gly Gln Asn Gln Ile Lys 175
 180 Val Thr Arg Cys Ser Ser Asp Ile Thr Gly Ile Phe Val Cys Glu Lys 190
 195 Gly Pro Cys Pro Gln Glu Asn Cys Ile Ile Ser Lys Leu Phe Lys Glu 205
 210 Gly Cys Thr Phe Ile Tyr Asn Ser Thr Gln Asn Ala Thr Ala Ser Ile 220
 225 Met Phe Met Gln Ser Leu Ser Ser Val Val Glu Phe Cys Asn Ala Ser 235
 245 Thr His Asn Gln Glu Ala Pro Asn Leu Gln Asn Gln Met Cys Ser Leu 250
 260 Arg Ser Ala Trp Asp Val Ile Thr Asp Ser Ala Asp Phe His His Ser 265
 275 Phe Pro Met Asn Gly Thr Glu Leu Pro Pro Pro Pro Thr Phe Ser Leu 285
 290 Val Glu Ala Gly Asp Lys Val Val Cys Leu Val Leu Asp Val Ser Ser 300
 305 Lys Met Ala Glu Ala Asp Arg Leu Leu Gln Leu Gln Gln Ala Ala Glu 315
 325 Phe Tyr Leu Met Gln Ile Val Glu Ile His Thr Phe Val Gly Ile Ala 330
 340 Ser Phe Asp Ser Lys Gly Glu Ile Arg Ala Gln Leu His Gln Ile Asn 345
 355 Ser Asn Asp Asp Arg Lys Leu Leu Val Ser Tyr Leu Pro Thr Thr Val 360
 370 Ser Ala Lys Thr Asp Ile Ser Ile Cys Ser Gly Leu Lys Lys Gly Phe 375
 385 Glu Val Val Glu Lys Leu Asn Gly Lys Ala Tyr Gly Ser Val Met Ile 390
 405 Leu Val Thr Ser Gly Asp Asp Lys Leu Leu Gly Asn Cys Leu Pro Thr 410
 420 Val Leu Ser Ser Gly Ser Thr Ile His Ser Ile Ala Leu Gly Ser Ser 425
 435 Ala Ala Pro Asn Leu Glu Glu Leu Ser Arg Leu Thr Gly Gly Leu Lys 440
 450 Phe Phe Val Pro Asp Ile Ser Asn Ser Asn Ser Met Ile Asp Ala Phe 455
 465 Ser Arg Ile Ser Ser Gly Thr Gly Asp Ile Phe Gln Gln His Ile Gln 460
 485 Leu Glu Ser Thr Gly Glu Asn Val Lys Pro His His Gln Leu Lys Asn 480
 500 Thr Val Thr Val Asp Asn Thr Val Gly Asn Asp Thr Met Phe Leu Val 495
 515 Thr Trp Gln Ala Ser Gly Pro Pro Glu Ile Ile Leu Phe Asp Pro Asp 510
 520 525

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Gly Arg Lys Tyr Tyr Thr Asn Asn Phe Ile Thr Asn Leu Thr Phe Arg				
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Thr Ala Ser Leu Trp Ile Pro Gly Thr Ala Lys Pro Gly His Trp Thr				
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Tyr Thr Leu Met Cys Phe His His Ala Lys Leu Leu Thr Trp Lys Leu				
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<210> 170

<211> 791

<212> PRT

<213> Homo sapiens

<400> 170

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	20	25	30	
Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn				
	35	40	45	
Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met				
	50	55	60	
Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val				
65	70	75	80	
Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Thr Trp Lys Ala Asn				
	85	90	95	
Asn Asn Ser Lys Ile Lys Gln Glu Ser Tyr Glu Lys Ala Asn Val Ile				
	100	105	110	
Val Thr Asp Trp Tyr Gly Ala His Gly Asp Asp Pro Tyr Thr Leu Gln				
	115	120	125	
Tyr Arg Gly Cys Gly Lys Glu Gly Lys Tyr Ile His Phe Thr Pro Asn				
	130	135	140	
Phe Leu Leu Asn Asp Asn Leu Thr Ala Gly Tyr Gly Ser Arg Gly Arg				
145	150	155	160	
Val Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe Asp Glu				
	165	170	175	
Tyr Asn Asn Asp Lys Pro Phe Tyr Ile Asn Gly Gln Asn Gln Ile Lys				
	180	185	190	
Val Thr Arg Cys Ser Ser Asp Ile Thr Gly Ile Phe Val Cys Glu Lys				
	195	200	205	
Gly Pro Cys Pro Gln Glu Asn Cys Ile Ile Ser Lys Leu Phe Lys Glu				
	210	215	220	
Gly Cys Thr Phe Ile Tyr Asn Ser Thr Gln Asn Ala Thr Ala Ser Ile				
225	230	235	240	
Met Phe Met Gln Ser Leu Ser Ser Val Val Glu Phe Cys Asn Ala Ser				
	245	250	255	
Thr His Asn Gln Glu Ala Pro Asn Leu Gln Asn Gln Met Cys Ser Leu				
	260	265	270	
Arg Ser Ala Trp Asp Val Ile Thr Asp Ser Ala Asp Phe His His Ser				
	275	280	285	
Phe Pro Met Asn Gly Thr Glu Leu Pro Pro Pro Pro Thr Phe Ser Leu				
	290	295	300	
Val Glu Ala Gly Asp Lys Val Val Cys Leu Val Leu Asp Val Ser Ser				
305	310	315	320	
Lys Met Ala Glu Ala Asp Arg Leu Leu Gln Leu Gln Gln Ala Glu				
	325	330	335	
Phe Tyr Leu Met Gln Ile Val Glu Ile His Thr Phe Val Gly Ile Ala				

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 Ser Phe Asp Ser Lys Gly Glu Ile Arg Ala Gln Leu His Gln Ile Asn
 355 360 365
 Ser Asn Asp Asp Arg Lys Leu Val Ser Tyr Leu Pro Thr Thr Val
 370 375 380
 Ser Ala Lys Thr Asp Ile Ser Ile Cys Ser Gly Leu Lys Lys Gly Phe
 385 390 395 400
 Glu Val Val Glu Lys Leu Asn Gly Lys Ala Tyr Gly Ser Val Met Ile
 405 410 415
 Leu Val Thr Ser Gly Asp Asp Lys Leu Leu Gly Asn Cys Leu Pro Thr
 420 425 430
 Val Leu Ser Ser Gly Ser Thr Ile His Ser Ile Ala Leu Gly Ser Ser
 435 440 445
 Ala Ala Pro Asn Leu Glu Glu Leu Ser Arg Leu Thr Gly Gly Leu Lys
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 465 470 475 480
 Ser Arg Ile Ser Ser Gly Thr Gly Asp Ile Phe Gln Gln His Ile Gln
 485 490 495
 Leu Glu Ser Thr Gly Glu Asn Val Lys Pro His His Gln Leu Lys Asn
 500 505 510
 Thr Val Thr Val Asp Asn Thr Val Gly Asn Asp Thr Met Phe Leu Val
 515 520 525
 Thr Trp Gln Ala Ser Gly Pro Glu Ile Ile Leu Phe Asp Pro Asp
 530 535 540
 Gly Arg Lys Tyr Tyr Thr Asn Asn Phe Ile Thr Asn Leu Thr Phe Arg
 545 550 555 560
 Thr Ala Ser Leu Trp Ile Pro Gly Thr Ala Lys Pro Gly His Trp Thr
 565 570 575
 Tyr Thr Leu Asn Asn Thr His His Ser Leu Gln Ala Leu Lys Val Thr
 580 585 590
 Val Thr Ser Arg Ala Ser Asn Ser Ala Val Pro Pro Ala Thr Val Glu
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 Ala Phe Val Glu Arg Asp Ser Leu His Phe Pro His Pro Val Met Ile
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 675 680 685
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 Pro Gly Ser His Ala Met Tyr Val Pro Gly Tyr Thr Ala Asn Gly Asn
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 Ile Gln Met Asn Ala Pro Arg Lys Ser Val Gly Arg Asn Glu Glu Glu
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 Arg Lys Trp Gly Phe Ser Arg Val Ser Ser Gly Gly Ser Phe Ser Val
 740 745 750
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 <211> 1491
 <212> DNA
 <213> Homo sapiens

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 <211> 364
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ser Pro Gly Arg Pro Arg Glu Leu Thr Ile Pro Gln Thr Ser Ser His
 50 55 60
 Gly Ala Asn Arg Phe Val Pro Lys Ser Lys Ala Leu Glu Ala Val Lys
 65 70 75 80
 Leu Ala Ile Glu Ala Gly Phe His His Ile Asp Ser Ala His Val Tyr
 85 90 95
 Asn Asn Glu Glu Gln Val Gly Leu Ala Ile Arg Ser Lys Ile Ala Asp
 100 105 110
 Gly Ser Val Lys Arg Glu Asp Ile Phe Tyr Thr Ser Lys Leu Trp Ser
 115 120 125
 Asn Ser His Arg Pro Glu Leu Val Arg Pro Ala Leu Glu Arg Ser Leu
 130 135 140
 Lys Asn Leu Gln Leu Asp Tyr Val Asp Leu Tyr Leu Ile His Phe Pro


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<210> 174

<211> 238

<212> PRT

<213> Homo sapiens

<400> 174

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      35             40             45
Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro Leu Leu Leu
      50             55             60
Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly Arg Gly Trp
      65             70             75             80
Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp Trp Lys Cys
      85             90             95
Ser Gln Glu Gly Gly Ser Gly Ser Tyr Glu Glu Gly Cys Gln Ser
      100            105            110
Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met Leu Phe Cys
      115            120            125
Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu
      130            135            140
Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu
      145            150            155            160
Ala Leu Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val
      165            170            175
Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Pro Ala Val Thr Tyr
      180            185            190
Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu
      195            200            205
Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp
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Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser Ala
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<210> 175

<211> 4181

<212> DNA

<213> Homo sapiens

<220>

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4036, 4056, 4062, 4080, 4088, 4115
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<210> 176

<211> 579

<212> PRT

<213> Homo sapiens

<400> 176

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Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
 35          40          45
Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
 50          55          60
Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile
 65          70          75          80
Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
 85          90          95
Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln
100          105          110
Val Asn Thr Asp Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Ser
115          120          125
Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu
130          135          140
Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Met Ala Ala
145          150          155          160
Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln
165          170          175
Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys
180          185          190
Pro Cys Asp Leu Pro Leu Arg Leu Leu Val Pro Thr Gln Phe Val Gly
195          200          205
Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
210          215          220
Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
225          230          235          240
Glu Lys Ser Ile Thr Ile Leu Ser Thr Pro Glu Gly Thr Ser Ala Ala
245          250          255
Cys Lys Ser Ile Leu Glu Ile Met His Lys Glu Ala Gln Asp Ile Lys
260          265          270
Phe Thr Glu Glu Ile Pro Leu Lys Ile Leu Ala His Asn Asn Phe Val

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275 280 285
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 290 295 300
 Asp Thr Asp Thr Lys Ile Thr Ile Ser Pro Leu Gln Glu Leu Thr Leu
 305 310 315 320
 Tyr Asn Pro Glu Arg Thr Ile Thr Val Lys Gly Asn Val Glu Thr Cys
 325 330 335
 Ala Lys Ala Glu Glu Ile Met Lys Lys Ile Arg Glu Ser Tyr Glu
 340 345 350
 Asn Asp Ile Ala Ser Met Asn Leu Gln Ala His Leu Ile Pro Gly Leu
 355 360 365
 Asn Leu Asn Ala Leu Gly Leu Phe Pro Pro Thr Ser Gly Met Pro Pro
 370 375 380
 Pro Thr Ser Gly Pro Pro Ser Ala Met Thr Pro Pro Tyr Pro Gln Phe
 385 390 395 400
 Glu Gln Ser Glu Thr Glu Thr Val His Gln Phe Ile Pro Ala Leu Ser
 405 410 415
 Val Gly Ala Ile Ile Gly Lys Gln Gly Gln His Ile Lys Gln Leu Ser
 420 425 430
 Arg Phe Ala Gly Ala Ser Ile Lys Ile Ala Pro Ala Glu Ala Pro Asp
 435 440 445
 Ala Lys Val Arg Met Val Ile Ile Thr Gly Pro Pro Glu Ala Gln Phe
 450 455 460
 Lys Ala Gln Gly Arg Ile Tyr Gly Lys Ile Lys Glu Glu Asn Phe Val
 465 470 475 480
 Ser Pro Lys Glu Glu Val Lys Leu Glu Ala His Ile Arg Val Pro Ser
 485 490 495
 Phe Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu
 500 505 510
 Leu Gln Asn Leu Ser Ser Ala Glu Val Val Val Pro Arg Asp Gln Thr
 515 520 525
 Pro Asp Glu Asn Asp Gln Val Val Val Lys Ile Thr Gly His Phe Tyr
 530 535 540
 Ala Cys Gln Val Ala Gln Arg Lys Ile Gln Glu Ile Leu Thr Gln Val
 545 550 555 560
 Lys Gln His Gln Gln Gln Lys Ala Leu Gln Ser Gly Pro Pro Gln Ser
 565 570 575
 Arg Arg Lys

<210> 177
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 177
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 agatccaaac aaatacacat tctgtgtttt agctcagttt ttcttaaaaa aagaaactgc 120
 cacacagcaa aaaattgttt actttgttgg acaaaccaaa tcagttctca aaaaatgacc 180
 ggtgcttata aaaagttata aatatcgagt agctctaaaa caaaccacct gaccaagag 240
 gaagtgaact tgtgcttagt atttacattg gatgccagtt ttgtaatcac tgacttatgt 300
 gcaaaactgt gcagaaattc tataaactct ttgctgtttt tgatacctgc ttttgtttc 360
 attttgtttt gttttgtaaa aatgataaaa cttcagaaaa t 401

<210> 178
 <211> 561
 <212> DNA

<213> Homo sapiens

<400> 178

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agtgagctgg ccaactgCGGT taaagcacga attgggagct ctacgcgaca tcaccagtca 180
gcagccaaag acctaaactca gtcccttgag gtctcccaa caaccatcca ggtgacatac 240
ctcccctcca gtcagaagag taaacgtgcc aagcacttcc ttgaattgaa gagctttaag 300
gataactata acacattgga gactactctg tgacggagct gaaggactct tgccgtagat 360
taagccagtc agttgcaatg tgcaagacag gctgcttgcc gggccgccc cggaaacatc 420
ggcccagcag gccagactg tatccatcca agttcccgtt gtatccagag ttcttagagc 480
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gactattttc cccagtagc g                                     561
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<210> 179

<211> 521

<212> DNA

<213> Homo sapiens

<400> 179

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gatcgagcaa tggcttcagg acatgggttc tcttctcctg tgatcattca agtgcctact 120
gcatgaagac tggcttgtct cagtgtttca acctcaccag ggctgtctct tgggccacac 180
ctcgctccct gttagtgcg tatgacagcc cccatcaaat gaccttgcc aagtcacggt 240
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acgtgagcag tcagcaccag ttctgcacca gcagcgctc cgtcctagtg ggtgttcctg 360
tttctcctgg ccctgggtgg gctagggcct gattcgggaa gatgccttg cagggagggg 420
aggataagtg ggatctacca attgattctg gcaaaacaat ttctaagatt tttttgcttt 480
atgtgggaaa cagatctaaa tctcatttta tgctgtattt t                                     521
```

<210> 180

<211> 417

<212> DNA

<213> Homo sapiens

<400> 180

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ggtggaattc gccgaagatg gcggagggtgc aggtcctggt gcttgatggt cgaggccatc 60
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tggctttcct ccgcaagcgg atgaacacca acccttccc agggccctac cacttccggg 240
ccccagccg catcttctg cggaacgtgc gaggtatgct gcccacaaa accaagcgag 300
gccaggccgc tctggaccgt ctcaaggtgt ttgacggcat cccaccgcc tacgacaaga 360
aaaagcggat ggtggttctt gctgccctca aggtcgtgcg tctgaagcct acaagaa 417
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<210> 181

<211> 283

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 35

<223> n = A,T,C or G

<400> 181

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caagaactca agtgaactg tgataaaata acctttcca ggtatattgg caggtatgtg 120
tgtaatctca gaatacacag gtgacataga tatgatatga caactggtaa tgggtgattc 180
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atttacattg tttacacttc tatgaccagg ccttaagggg aggtcagttt tttaaaaaac 240
caagtagtgt cttcctacct atctccagat acatgtcaaa aaa 283

<210> 182

<211> 401

<212> DNA

<213> Homo sapiens

<400> 182

atattcttgc tgccttatgca gctgacattg ttgccctccc taaagcaacc aagtagcctt 60
tatttcccac agtgaagaa aacgctggcc tatcagttac attacaaaag gcagatttca 120
agaggattga gtaagtagtt ggatggcttt cataaaaaa agaattcaag aagaggattc 180
atgctttaag aaacatttgt tatacattcc tcacaaatta tacctgggat aaaaactatg 240
tagcaggcag tgtgttttcc ttccatgtct ctctgcacta cctgcagtgt gtcctctgag 300
gctgcaagtc tgcctatct gaattcccag cagaagcact aagaagctcc accctatcac 360
ctagcagata aaactatggg gaaaacttaa atctgtgcat a 401

<210> 183

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 325

<223> n = A,T,C or G

<400> 183

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gtgtcggaat cactggtaaa tgttggtctga gaacaatccc tccccttgca ctgtgaaaa 300
cactttgagc gctttaagag attancctga gaaataatta aatatctttt ctcttcaaaa 360
aaaaaa 366

<210> 184

<211> 370

<212> DNA

<213> Homo sapiens

<400> 184

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tttaataatt gtactgagag aaactgctta cgtacacatt gcagatcaaa tatttgagat 120
taaaatgtta gtctacatag atgggtgatt gtaactttat tgccattaaa agatttcaaa 180
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tcagtctgct ctgtttaatt ctgctgtctg ctcttctcta atgctgcgtc cctaattgta 300
cacagtttag tgatatctag gagtataaag ttgtcgcca tcaataaaaa tcacaaagtt 360
ggtttaaaaa 370

<210> 185

<211> 107

<212> DNA

<213> Homo sapiens

<400> 185

ctcatattat tttccttttg agaaattgga aactctttct gttgctatta tattaataaa 60
gttggtgttt attttctggt agtcaccttc cccatttaaa aaaaaaa 107

<210> 186
<211> 309
<212> DNA
<213> Homo sapiens

<400> 186
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gccagtgagt gacagtcacg agggagtgtc tcttcttggg gaggaagaa ggtagagcct 180
ttctgtctga atgaaaggcc aaggctacag tacagggccc cgccccagcc aggggtgttaa 240
tgcccacgta gtggaggcct ctggcagatc ctgcattcca aggtcactgg actgtacgtt 300
tttatggtt 309

<210> 187
<211> 477
<212> DNA
<213> Homo sapiens

<400> 187
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atgtcttcag aagcaagtca ggtttcatgt aaccgagtgt cctcttgcgt gtccaaaagt 420
agcccagggc tgtagcacag gcttcacagt gatthttgtgt tcagccgtga gtcacac 477

<210> 188
<211> 220
<212> DNA
<213> Homo sapiens

<400> 188
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cagatgttca agaggaagtt gctattgcat tgattttaat atttgtacat aaacactgat 180
ttttttgagc attattttgt atttgttgta ctttaatacc 220

<210> 189
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 76, 77
<223> n = A,T,C or G

<400> 189
accatcttga cagaggatac atgctcccaa aacgtttgtt accacactta aaaatcactg 60
ccatcattaa gcatcnnttt caaaattata gccattcatg atttactttt tccagatgac 120
tatcattatt ctagtccttt gaatttgtaa ggggaaaaaa aacaaaaaca aaaacttacg 180
atgcactttt ctccagcaca tcagatttca aattgaaaat taaagacatg ctatggtaat 240
gcacttgcta gtactacaca ctttgtacaa caaaaaacag aggcaagaaa caacggaaaag 300
agaaaagcct tcctttgttg gcccttaaac tgagtcaaga tctgaaatgt agagatgatc 360
tctgacgata cctgtatgtt cttattgtgt aaataaaaatt gctggtatga aatgaca 417

<210> 190
<211> 497
<212> DNA
<213> Homo sapiens

<400> 190
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aacgcaggag ctgtcattga ctggcccaca gaggagggca aggaagtatg ggattatgtg 120
acggtccgca aggatgccta catgttctgg tggctctatt atgccaccaa ctctgcaag 180
aacttctcag aactgcccct ggtcatgtgg cttcagggcg gtccaggcgg ttctagcact 240
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tatgtgaatg gtagtggtgc ctatgccaa gacctggcta tgggtggctc agacatgatg 420
gttctcctga agaccttctt cagttgccac aaagaattcc agacagttcc attctacatt 480
ttctcagagt cctatgg 497

<210> 191
<211> 175
<212> DNA
<213> Homo sapiens

<400> 191
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ctacttgagt acaaggattt gagcctgtta cattcactgc tgaatttttag gctcctggaa 120
gatacccagc attcaataga gaccacacaa taaatatatg tcaataaaaa aaaaa 175

<210> 192
<211> 526
<212> DNA
<213> Homo sapiens

<400> 192
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aagaacagta ttgctgtaat tccttttctt ttcttctca tttcctctgc cccttaaaag 120
attgaagaaa gagaaacttg tcaactcata tccacgttat ctacaaagt acataagaat 180
ctatcactaa gtaatgtatc cttcagaatg tgttgggtta ccagtgcac cccatattca 240
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tcagagtttc tgaggtaaaa ttttatctt tcaattaca gctctatgat cttaataat 360
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<210> 193
<211> 553
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 290, 300, 411, 441
<223> n = A,T,C or G

<400> 193
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gctgggatga gccgtgctcc cgggtggaagc aaggagccc agccggagcc atggccagta 120
cagtggttagc agttggactg accattgctg ctgcaggatt tgcaggccgt tacgttttgc 180
aagccatgaa gcatatggag cctcaagtaa aacaagtttt tcaaagccta ccaaaatctg 240

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ccttcagtgg tggctattat agaggtgggt ttgaacccaa aatgacaaan cgggaagcan 300
cattaatact aggtgtaagc cctactgcca ataaagggaa aataagagat gctcatcgac 360
gaattatgct tttaaatcat cctgacaaag gaggatctcc ttatatagca nccaaaatca 420
atgaagctaa agatttacta naaggtcaag ctaaaaaatg aagtaaattgt atgatgaatt 480
ttaagtctgt attagtttat gtatatgagt actaagtttt tataataaaa tgcctcagag 540
ctacaatttt aaa 553

```

```

<210> 194
<211> 320
<212> DNA
<213> Homo sapiens

```

```

<400> 194
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attaagactc tgataattgt ctcccctcca taggaatttc tcccaggaaa gaaatatatc 180
cccattctcg ttctatatec gaactaccgt ccccgatatt cccttcagag agattaaaga 240
ccagaaaaaa gtgagcctct tcatctgcac ctgtaatagt ttcagttcct attttcttcc 300
attgacccat atttatacct 320

```

```

<210> 195
<211> 320
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 203, 218
<223> n = A,T,C or G

```

```

<400> 195
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gtgaccagaa tctgccatgg caacaggcct taaaaaagac ccttaaaaag acactgtctc 120
aactgtggtg tttagcaccag ccagctctct gtacatttgc tagctttagt ttttctaaga 180
ctgagtaaac ttcttatttt tanaaagggg aggcgtgntt gtaactttcc ttgtacttaa 240
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tatttggtaa attatgaact 320

```

```

<210> 196
<211> 357
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> 36
<223> n = A,T,C or G

```

```

<400> 196
atataaaaata atacgaaact ttaaaaagca ttggantgtc agtatgttga atcagtagtt 60
tcactttaac tgtaaacaaat ttcttaggac accatttggg ctagtcttct tgtaagtgtg 120
aatactacaa aaacttattt atactgttct tatgtcattt gttatattca tagatttata 180
tgatgatatg acatctggct aaaaagaaat tattgcaaaa ctaaccacta tgtacttttt 240
tataaatact gtatggacaa aaaatggcat tttttatatt aaattgttta gctctggcaa 300
aaaaaaaaaa ttttaagagc tgggtactaat aaaggattat tatgactgtt aaaaaaa 357

```

```

<210> 197
<211> 565

```

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 27

<223> n = A,T,C or G

<400> 197

```

tcagctgagt accatcagga tatttanccc ttttaagtgt gttttgggag tagaaaaacta 60
aagcaacaat acttcctctt gacagctttg attggaatgg ggttattaga tcattcacct 120
tggtcctaca ctttttagga tgcttggtga acataacacc acttataatg aacatccctg 180
gttcctatat tttgggctat gtgggtagga attgttactt gttactgcag cagcagccct 240
agaaagtaag cccagggctt cagatctaag ttagtccaaa agctaaatga tttaaagtca 300
agttgtaatg ctaggcataa gcaacttata atacattaaa ttataggccg agcaattagg 360
gaatgtttct gaaacattaa acttgtatct atgtcactaa aattctaaca caaacttaaa 420
aaatgtgtct catacatatg ctgtactagg cttcatcatg ctttctaaa tttgtgtatg 480
atttgaatat atgaaagaat ttatacaaga gtgttattta aaattattaa aaataaatgt 540
atataatttg tacctattgt aaaaaa

```

565

<210> 198

<211> 484

<212> DNA

<213> Homo sapiens

<400> 198

```

tatgtaagta ttggtgtctg ctttaaaaaa ggagaccag acttcacctg tcctttttta 60
acatttgaga acagtgttac tctgagcagt tgggccacct tcaccttacc cgacagctga 120
ctgttggtatg tgtccattgt cgccagtttg gctgttgccc ggacaggaca ggacctccat 180
tgggcgcagc agcaggtggc aggggtgtgg cttgaggtgg gtggcagcgt ctggctcctc 240
tctctggtgc tttctgagag ggtctctaaa gcagagtgtg gttggcctgg gggaaggcag 300
agcagctatt tctccctct agtacctctg catttgtagg tggtccctct ggctttctga 360
agggcagcag actcttgagt atactgcaga ggacatgctt tatcagtagg tcctgagggc 420
tccaggggct caactgacca agtaacacag aagttggggg atgtggccta tttgggtcgg 480
aaac

```

484

<210> 199

<211> 429

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 77, 88, 134, 151, 189, 227, 274, 319

<223> n = A,T,C or G

<400> 199

```

gcttatgttt tttgttttaa cttttgtttt ttaacattta gaatattaca ttttgtatta 60
tacagtacct ttctcanaca ttttgtanaa ttcatttcgg cagctcacta ggattttgct 120
gaacattaaa aagngtgata gcgatattag ngccaatcaa atggaaaaaa ggtagtctta 180
ataaacaana cacaacgttt ttatacaaca tactttaaaa tattaanaaa actccttaat 240
attgtttcct attagatttt attcctttggg caanattttc tgatgctttt gattttctct 300
caatttagca tttgctttng gtttttttct ctatttagca ttctgttaag gcacaaaaac 360
tatgtactgt atgggaaatg ttgtaaatat taccttttcc acattttaaa cagacaactt 420
tgaatccaa

```

429

<210> 200

<211> 279

<212> DNA

<213> Homo sapiens

<400> 200

```

gcttttttga ggaattacag ggaagctcct ggaattgtac atggatatct ttatccctag 60
ggggaaatca aggagctggg caccctaata tctttatgga agtggtttaaa actatttttaa 120
ttttattaca agtattacta gagtagtggt tctactctaa gatttcacaaa gtgcatttaa 180
aatcatacat gttcccgctt gcaaatatat tgttattttg gtggagaaaa aaatagtata 240
ttctacataa aaaattaaag atattaacta agaaaaaaa 279

```

<210> 201

<211> 569

<212> DNA

<213> Homo sapiens

<400> 201

```

taggtcagta tttttagaaa ctcttaatag ctcatactct tgataccaaa agcagccctg 60
attgttaaag cacacacctg cacaagaagc agtgatgggt gcattttacat ttcctgggtg 120
cacaaaaaaa aattctcaaa aagcaaggac ttacgctttt tgcaaagcct ttgagaagtt 180
actggatcat aggaagctta taacaagaat ggaagattct taaataactc actttctttg 240
gtatccagta acagtagatg ttcaaaatat gtagctgatt aataccagca ttgtgaacgc 300
tgtacaacct tgtgggttatt actaagcaag ttactactag cttctgaaaa gtagcttcat 360
aattaatggt atttatacac tgccttccat gacttttact ttgccctaag ctaatctcca 420
aaatctgaaa tgctactcca atatcagaaa aaaaggggga ggtggaatta tatttcctgt 480
gatttttaaga gtacagagaa tcatgcacat ctctgattag ttcatatatg tctagtgtgt 540
aataaaagtc aaagatgaac tctcaaaaa 569

```

<210> 202

<211> 501

<212> DNA

<213> Homo sapiens

<400> 202

```

attaatagtc ttaataattg ttggcaagga tccttttgct ttctttggca tgcaagctcc 60
tagcatctgg cagtggggcc aagaaaataa ggtttatgca tgtatgatgg ttttcttctt 120
gagcaacatg attgagaacc agtgatatgc aacagggtgca tttgagataa ctttaaataa 180
tgtacctgtg tggctctaagc tggaatctgg tcaccttcca tccatgcaac aacttggtta 240
aattcttgac aatgaaatga agctcaatgt gcatatggat tcaatccac accatcgatc 300
atagcaccac ctatcagcac tgaaaactct tttgcattaa gggatcattg caagagcagc 360
gtgactgaca ttatgaaggc ctgtactgaa gacagcaagc tgtagtagta gaccagatgc 420
tttcttggca ggctcgttgt acctcttgga aaacctcaat gcaagatagt gtttcagtgc 480
tggcatatct tgggaattctg c 501

```

<210> 203

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 36, 96

<223> n = A,T,C or G

<400> 203

```

gacaagctcc tggctctgag atgtcttctc gttaangaga tgggcctttt ggaggttaaag 60
gataaaatga atgagttctg tcatgattca ctatntata acttgcatga cctttactgt 120
gttagctctt tgaatgttct tgaaatttta gactttcttt gtaaacaat gatatgtcct 180
tatcattgta taaaagctgt tatgtgcaac agtgtggaga ttccttgtct gatttaataa 240

```

aataacttaaa cactgaaaaa a

261

<210> 204

<211> 421

<212> DNA

<213> Homo sapiens

<400> 204

agcatctttt ctacaacggt aaaattgcag aagtagctta tcattaaaaa acaacaacaa 60
caacaataac aataaatcct aagtgtaaat cagttattct accccctacc aaggatatca 120
gcctgttttt tccctttttt ctccctggga taattgtggg cttcttccca aatttctaca 180
gcctctttcc tcttctcatg cttgagcttc cctgtttgca cgcacgcgtg tgcaggactg 240
gcttgtgtgc ttggactcgg ctccagggtg aagcatgctt tcccttggtt ctgttgga 300
aactcaaacc ttcaagccct aggtgtagcc atttgtcaa gtcacaaact gtatttttgt 360
actggcatta acaaaaaaag aagataaaat attgtaccat taaactttaa taaaacttta 420
a 421

<210> 205

<211> 460

<212> DNA

<213> Homo sapiens

<400> 205

tactctcaca atgaaggacc tggaatgaaa aatctgtgtc taaacaagtc ctctttagat 60
tttagtgcaa atccagagcc agcgtcggtt gcctcgagta attctttcat gggtagcttt 120
ggaaaagctc tcaggagacc tcacctagat gcctattcaa gctttggaca gccatcagat 180
tgtcagccaa gagcctttta ttgaaagct cattcttccc cagacttggg ctctgggtca 240
gaggaagatg ggaagaaaag gacagatttt caggaagaaa atcacatttg tacctttaaa 300
cagactttag aaaactacag gactccaaat tttagctctt atgacttggg cacatagact 360
gaatgagacc aaaggaaaag cttaacatac tacctcaagg tgaactttta tttaaaagag 420
agagaatctt atgtttttta aatggagtta tgaattttaa 460

<210> 206

<211> 481

<212> DNA

<213> Homo sapiens

<400> 206

tgtggtggaa ttcgggacgc ccccagaccc tgactttttc ctgcgtgggc cgtctcctcc 60
tgcggaagca gtgacctctg acccttggtg accttcgctt tgagtgcctt ttgaacgctg 120
gtcccgcggtg acttggtttt ctcaagctct gtctgtccaa agacgctccg gtcgaggtcc 180
cgctgcctt ggggtggatac ttgaacccca gacgcccctc tgtgctgctg tgcgggagg 240
cgcccttccc atctgcctgc ccaccggag ctctttccgc cggcgaggg tcccaagccc 300
acctcccgcc ctgagtcctg cgggtgtcgt ctgggcacgt cctgcacaca caatgcaagt 360
cctggcctcc ggcgccgccc gccacgcga gccgtaccgc ccgccaactc tgttatttat 420
ggtgtgaccc cctggagggtg cctcggccc accggggcta tttattggtt aatttatttg 480
t 481

<210> 207

<211> 605

<212> DNA

<213> Homo sapiens

<400> 207

accctttttg gattcagggc tcttcacaat taaaatgagt gtaatgaaac aaggtgaaaa 60
tatagaagca tccctttgta tactgttttg ctacttacag tgtacttggc attgctttat 120
ctcactggat tctcacggta ggatttctga gatcttaac taagctccaa agttgtctac 180
ttttttgatc ctagggtgct ccttttgttt tacagagcag ggtcacttga tttgctagct 240


```

ggtggcagaa ttggcaccat taccaggtc tgactgacca ccagtcagag gcactttatt 300
tgtatcatga aatgatttga aatcattgta aagcagcgaa gtctgataat gaatgccagc 360
tttcttcttg ctttgataac aaagactcca aatattctgg agaactgga taaaagtttg 420
aagggctaga ttgggatttg aagacaaaat tgtaggaaat ctacattttt tgcaataaca 480
aacattaatg aaagcaaac attataaaag taattttaat tcaccacata cttatcaatt 540
tcttgatgct tccaaatgac atctaccaga tatggttttg tggacatctt tttctgttta 600
cataa 605

```

<210> 208

<211> 655

<212> DNA

<213> Homo sapiens

<400> 208

```

ggcgttggtc tggattcccg tcgtaactta aagggaaact ttcacaatgt ccggagccct 60
tgatgtcctg caaatgaagg aggaggatgt ccttaagtcc ctgacagcag gaaccactt 120
aggtggcacc aatcttgact tccagatgga acagtacatc tataaaagga aaagtgatgg 180
catctatatc ataaatctca agaggacctg ggagaagctt ctgctggcag ctctgcaat 240
tgttgccatt gaaaacctg ctgatgtcag tggtatatcc tccaggaata ctggccagag 300
ggctgtgctg aagtttgctg ctgccactgg agccactcca attgctggcc gcttactcc 360
tggaaccttc actaaccaga tccaggcagc cttccgggag ccacggcttc ttgtggttac 420
tgacccacag gctgaccacc agcctctcac ggaggcatct tatgttaacc tacctacat 480
tgcgctgtgt aacacagatt ctctctgctg ctatgtggac attgccatcc catgcaacaa 540
caagggagct cactcagtg gtttgatgtg gtggatgctg gctcgggaag ttctgcgcac 600
gcgtggcacc atttcccgtg aacacccatg ggaggtcatg cctgatctgt acttc 655

```

<210> 209

<211> 621

<212> DNA

<213> Homo sapiens

<400> 209

```

catttagaac atggttatca tccaagacta ctctaccctg caacattgaa ctccaagag 60
caaatccaca ttctcttga gttctgcagc ttctgtgtaa atagggcagc tgcgtctat 120
gccgtagaat cacatgatct gaggaccatt catggaagct gctaaatagc ctagtctggg 180
gagtcttcca taaagttttg catggagcaa acaaacagga ttaactagg tttggttcct 240
tcagccctct aaaagcatag ggcttagcct gcaggcttcc ttgggcttcc tctgtgtgtg 300
tagttttgta aacactatag catctgttaa gatccagtgt ccatggaaac cttcccat 360
gccgtgactc tggactatat cagtttttgg aaagcagggt tcctctgcct gctaacaagc 420
ccacgtggac cagtctgaat gtctttcctt tacacctatg tttttaata gtcaaacttc 480
aagaaacaat ctaaacaagt ttctgttgca tatgtgtttg tgaacttgta tttgtattta 540
gtaggcttct atattgcatt taacttgttt ttgtaactcc tgattcttcc ttttcggata 600
ctattgatga ataaagaaat t 621

```

<210> 210

<211> 533

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 20, 21, 61

<223> n = A,T,C or G

<400> 210

```

cgccttgggg agccggcggn ngagtccggg acgtggagac ccgggggtccc ggcagccggg 60
ngggcccgcg gccaggggtg gggatgcacc gccgcggggt gggagctggc gccatcgcca 120
agaagaaact tgcagaggcc aagtataagg agcgaggagc ggtcttggct gaggaccagc 180

```

tagcccagat gtcaaagcag ttggacatgt tcaagaccaa cctggaggaa tttgccagca 240
aacacaagca ggagatcccg aagaatcctg agttccgtgt gcagttccag gacatgtgtg 300
caaccattgg cgtggatccg ctggcctctg gaaaaggatt ttggtctgag atgctgggcg 360
tgggggactt ctattacgaa ctaggtgtcc aaattatcga agtgtgcctg gcgctgaagc 420
atcggaatgg aggtctgata actttggagg aactacatca acaggtgttg aagggaaggg 480
gcaagttcgc ccaggatgtc agtcaagatg acctgatcag agccatcaag aaa 533

<210> 211

<211> 451

<212> DNA

<213> Homo sapiens

<400> 211

ttagcttgag ccgagaacga ggcgagaaag ctggagaccg aggagaccgc ctagagcgga 60
gtgaacgggg aggggaccgt ggggaccggc ttgatcgtgc gcggacacct gctaccaagc 120
ggagcttcag caaggaagtg gaggagcgga gtagagaacg gccctcccag cctgaggggc 180
tgcgcaaggc agctagcctc acggaggatc gggaccgtgg gcgggatgcc gtgaagcgag 240
aagctgccct acccccagtg agccccctga aggcggctct ctctgaggag gaggtagaga 300
agaaatccaa ggctatcatt gaggaatata tccatctcaa tgacatgaaa gaggcagtcc 360
agtgcgtgca ggagctggcc tcaccctcct tgctcttcat ctttgtacgg catggtgtcg 420
agtctacgct ggagcgcagt gccattgctc g 451

<210> 212

<211> 471

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 54

<223> n = A,T,C or G

<400> 212

gtgattattc ttgatcaggg agaagatcat ttagatttgt tttgcattcc ttanaatgga 60
gggcaacatt ccacagctgc cctggctgtg atgagtgtcc ttgcaggggc cggagtagga 120
gcactggggg gggggcggaa ttggggttac tcgatgtaag ggattccttg ttgttgtgtt 180
gagatccagt gcagttgtga tttctgtgga tcccagcttg gttccaggaa ttttgtgtga 240
ttggcttaaa tccagtttcc aatcttcgac agctgggctg gaacgtgaac tcagtagctg 300
aacctgtctg acccggtcac gttcttggat cctcagaact ctttgccttt gtcgggggtg 360
gggtgggaac tcacgtgggg agcgggtggc gagaaaatgt aaggattctg gaatacatat 420
tccatgggac tttccttccc tctcctgctt cctcttttcc tgctccctaa c 471

<210> 213

<211> 511

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 27, 63, 337, 442

<223> n = A,T,C or G

<400> 213

ctaattagaa acttgctgta cttttnttt tcttttaggg gtcaaggacc ctctttatag 60
ctnccatttg cctacaataa attattgcag cagtttgcaa tactaaaata ttttttatag 120
actttatatt tttccttttg ataaagggat gctgcatagt agagttggtg taattaaact 180
atctcagccg tttccctgct ttcccttctg ctccatagtc ctcatgtcc ttccaggag 240
ctcttttaat cttaaagttc tacatttcat gctcttagtc aaattctgtt acctttttaa 300

```
taactcttcc cactgcatat ttccatcttg aattgngngt tctaaattct gaaactgtag 360
ttgagataca gctattttaat atttctggga gatgtgcac cctcttcttt gtggttgccc 420
aagggttgtt tgcgtaactg anactccttg atatgcttca gagaatttag gcaaactg 480
gccatggccg tgggagtact gggagtaaaa t 511
```

<210> 214

<211> 521

<212> DNA

<213> Homo sapiens

<400> 214

```
agcattgcc aataatccct aattttccac taaaaatata atgaaatgat gttaagcttt 60
ttgaaaagt taggttaaac ctactgttgt tagattaatg tattgtgtgc ttccctttat 120
ctggaatgtg gcattagctt ttttatttta accctcttta attcttattc aattccatga 180
cttaaggttg gagagctaaa cactgggatt ttgggataac agactgacag ttttgcataa 240
ttataatcgg cattgtacat agaaaggata tggctacctt ttgttaaatac tgcactttct 300
aaatatcaaa aaagggaaat gaagtataaa tcaatttttg tataatctgt ttgaaacatg 360
agtttttatt gcttaatat agggctttgc ccttttctg taagtctctt gggatcctgt 420
gtagaagctg ttctcattaa acaccaaaca gttaagtcca ttctctggta ctagctaaa 480
attcggtttc atattctact taacaattta aataaactga a 521
```

<210> 215

<211> 381

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 17, 20, 60, 61, 365

<223> n = A,T,C or G

<400> 215

```
gagcggagag cggaccngtn agagccctga gcagcccccac cgccgccgcc ggcctagttn 60
ncatcacacc cggggaggag ccgcagctgc cgcagccggc cccagtcacc atcacgcaa 120
ccatgagcag cgaggccgag acccagcagc cgcccgcgc ccccccgcc gccccgccc 180
tcagcgccgc cgacaccaag cccggcacta cgggcagcgc cgcagggagc ggtggcccg 240
gcggcctcac atcggcggcg cctgccggcg gggacaagaa ggtcatcgca acgaaggtt 300
tggaacagat aaaatggtc aatgtaagga acggatatgg ttcatcaac aggaatgaca 360
ccaangaaga tgtatttgta c 381
```

<210> 216

<211> 425

<212> DNA

<213> Homo sapiens

<400> 216

```
ttactaacta ggtcattcaa ggaagtcaag ttaacttaaa catgtcacct aaatgcactt 60
gatggtgttg aaatgtccac ctctttaa attttaagatg aacttagttc taaagaagat 120
aacaggccaa tcctgaaggt actccctgtt tgctgcagaa tgtcagatat tttggatgtt 180
gcataagagt cctatttgcc ccagttaatt caacttttgt ctgcctgttt tgtggactgg 240
ctggctctgt tagaactctg tccaaaaagt gcatggaata taacttgtaa agcttccac 300
aattgacaat atatatgcat gtgtttaaac caaatccaga aagcttaaac aatagagctg 360
cataatagta tttattaaag aatcacaact gtaaacaatga gaataactta aggattctag 420
tttag 425
```

<210> 217

<211> 181

<212> DNA

<213> Homo sapiens

<400> 217

```
gagaaaccaa atgatagggt gtagagcctg atgactccaa acaaagccat caccgcgatt 60
cttcctcctt cttctggtgc tacagctcca agggcccttc accttcatgt ctgaaatgga 120
actttggctt tttcagtga agaatatgtt gaaggtttca tttgttcta gaaaaaaaaa 180
a                                                                 181
```

<210> 218

<211> 405

<212> DNA

<213> Homo sapiens

<400> 218

```
caggccttcc agttcactga caaacatggg gaagtgtgcc cagctggctg gaaacctggc 60
agtgatacca tcaagcctga tgtccaaaag agcaaagaat atttctccaa gcagaagtga 120
gcgctgggct gtttttagtg caggctgcgg tgggcagcca tgagaacaaa acctcttctg 180
tatttttttt ttccattagt aaaacacaag acttcagatt cagccgaatt gtggtgtctt 240
acaaggcagg cctttcctac agggggtgga gagaccagcc tttcttcctt tggtaggaat 300
ggcctgagtt ggcgttggtg gcaggctact ggtttgtatg atgtattagt agagcaaccc 360
attaatcttt tgtagtttgt attaaacttg aactgagaaa aaaaaa                    405
```

<210> 219

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 207, 210

<223> n = A,T,C or G

<400> 219

```
actccaagag ttagggcagc agagtggagc gatttagaaa gaacatttta aaacaatcag 60
ttaatttacc atgtaaaatt gctgtaaatg ataattgtga cagattttct gttcaaatat 120
tcaattgtaa acttcttggt aagactgtta cgtttctatt gcttttgtat gggatattgc 180
aaaaataaaa aggaaagaac cctcttnaan aaaaaa                    216
```

<210> 220

<211> 380

<212> DNA

<213> Homo sapiens

<400> 220

```
cttacaaatt gcccccatgt gtaggggaca cagaaccctt tgagaaaact tagatttttg 60
tctgtacaaa gtctttgcct ttttccttct tcattttttt ccagtacatt aaatttgtca 120
atttcatctt tgagggaac tgattagatg ggtttgtgtt gtgttctgat ggagaaaaca 180
gcaccccaag gactcagaag atgattttta cagttcagaa cagatgtgtg caatattggt 240
gcatgtaata atgttgagtg gcagtcaaaa gtcagtattt ttatcttagt tcttcattac 300
tgcattgaaa aggaaaacct gtctgagaaa atgcctgaca gtttaattta aaactatggt 360
gtaagtcttt gacaaaaaaa                    380
```

<210> 221

<211> 398

<212> DNA

<213> Homo sapiens

<400> 221

```

ggtagtaag ctgtcgactt tgtaaaaaag ttaaaaatga aaaaaaaagg aaaaatgaat 60
tgtatattta atgaatgaac atgtacaatt tgccactggg aggagggtcc tttttgttgg 120
gtgagtcctgc aagtgaattt cactgatgtt gatattcatt gtgtgtagtt ttatttcggt 180
cccagccccg tttcctttta ttttggagct aatgccagct gcgtgtctag ttttgagtgc 240
agtaaaatag aatcagcaaa tcactcttat ttttcacctt tttccggtat tttttgggtt 300
gtttctgtgg gagcagtgtg caccaactct tcctgtatat tgcctttttg ctggaaaatg 360
ttgtatgttg aataaaattt tctataaaaa ttaaaaaa 398

```

<210> 222

<211> 301

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 49, 64

<223> n = A,T,C or G

<400> 222

```

ttcgataatt gatctcatgg gctttccctg gaggaaaggt tttttttgnt gtttattttt 60
taanaacttg aaacttgtaa actgagatgt ctgtagcttt ttgcccac tgtagtgtat 120
gtgaagattt caaaacctga gagcactttt tctttgttta gaattatgag aaaggcacta 180
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<212> DNA

<213> Homo sapiens

<400> 223

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<211> 385

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<211> 560

<212> PRT

<213> Homo sapiens

<400> 225

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 35 40 45
 Ser Asp Glu Asn Asp Trp Asn Glu Lys Leu Tyr Pro Val Trp Lys Arg
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 Gly Asp Met Arg Trp Lys Asn Ser Trp Lys Gly Gly Arg Val Gln Ala
 65 70 75 80
 Val Leu Thr Ser Asp Ser Pro Ala Leu Val Gly Ser Asn Ile Thr Phe
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 Ala Val Asn Leu Ile Phe Pro Arg Cys Gln Lys Glu Asp Ala Asn Gly
 100 105 110
 Asn Ile Val Tyr Glu Lys Asn Cys Arg Asn Glu Ala Gly Leu Ser Ala
 115 120 125
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 Pro Phe Pro His His Pro Gly Trp Arg Arg Trp Asn Phe Ile Tyr Val
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 Arg Val Ser Val Asn Thr Ala Asn Val Thr Leu Gly Pro Gln Leu Met
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 Gln Val Lys Asp Val Tyr Val Val Thr Asp Gln Ile Pro Val Phe Val
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 Lys Asp Leu Pro Ile Met Phe Asp Val Leu Ile His Asp Pro Ser His
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 Thr Gly Leu Phe Val Ser Thr Asn His Thr Val Asn His Thr Tyr Val
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 Gly Pro Cys Pro Pro Pro Pro Pro Pro Arg Pro Ser Lys Pro Thr
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 Asp Val Leu Met Pro Val Pro Trp Pro Glu Ser Ser Leu Ile Asp Phe
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 Ser Asp Pro Thr Cys Glu Ile Thr Gln Asn Thr Val Cys Ser Pro Val
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107

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Tyr	Asn	Pro	Ile	Glu	Asn	Ser	Pro	Gly	Asn	Val	Val	Arg	Ser	Lys	Gly
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<211> 20

<212> PRT

<213> Homo sapiens

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Asn Pro Gln Gln
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Phe Ile Pro Pro Asn
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Gln Ile Ser Thr
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<400> 240

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<212> PRT

<213> Homo sapiens

<400> 241

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Val	Leu	Gly	Val												
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<213> Homo sapiens

<400> 242

Gly	Ser	His	Ala	Met	Tyr	Val	Pro	Gly	Tyr	Thr	Ala	Asn	Gly	Asn	Ile
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Gln	Met	Asn	Ala												
				20											

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<212> PRT

<213> Homo sapiens

<400> 243

Val	Asn	His	Ser	Pro	Ser	Ile	Ser	Thr	Pro	Ala	His	Ser	Ile	Pro	Gly
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				20											

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<211> 20

<212> PRT

<213> Homo sapiens

<400> 244

Ala	Val	Pro	Pro	Ala	Thr	Val	Glu	Ala	Phe	Val	Glu	Arg	Asp	Ser	Leu
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His	Phe	Pro	His												
				20											

<210> 245

<211> 20

<212> PRT

<213> Homo sapiens

<400> 245

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Gln Ala Leu Lys
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<210> 246

<211> 20

<212> PRT

<213> Homo sapiens

<400> 246

Asn Leu Thr Phe Arg Thr Ala Ser Leu Trp Ile Pro Gly Thr Ala Lys
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Pro Gly His Trp
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<210> 247

<211> 20

<212> PRT

<213> Homo sapiens

<400> 247

Leu His Phe Pro His Pro Val Met Ile Tyr Ala Asn Val Lys Gln Gly
1 5 10 15
Phe Tyr Pro Ile
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<210> 248

<211> 20

<212> PRT

<213> Homo sapiens

<400> 248

Pro Glu Thr Gly Asp Pro Val Thr Leu Arg Leu Leu Asp Asp Gly Ala
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<210> 249

<211> 20

<212> PRT

<213> Homo sapiens

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 35 40 45
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 Ala Val Gly Leu Ser Ala Glu Ala Leu Thr Ile Gln Gln Tyr Ala Asp
 65 70 75 80
 Val Leu Ser Lys Ala Leu Gly Lys Glu Val Arg Asp Ala Lys Ile Thr
 85 90 95
 Pro Glu Ala Phe Glu Lys Leu Gly Phe Pro Ala Ala Lys Glu Ile Ala
 100 105 110
 Asn Met Cys Arg Phe Tyr Glu Met Lys Pro Asp Arg Asp Val Asn Leu
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ggaggaatta tcacgtctta caggagggtt aaagttcttt gtccagata tatcaaactc 6420
caatagcatg attgatgctt tcagtagaat ttctctgga actggagaca ttttccagca 6480
acatattcag cttgaaagta caggtgaaaa tgtcaaacct caccatcaat tgaaaaacac 6540
agtgactgtg gataatactg tgggcaacga cactatgttt ctagttacgt ggcaggccag 6600
tggtcctcct gagattatat tatttgatcc tgatggacga aaatactaca caaataattt 6660
tatcaccaat ctaacttttc ggacagctag tctttggatt ccaggaacag ctaagcctgg 6720
gcactggact tacaccctga acaataccca tcattctctg caagccctga aagtgcagct 6780
gacctctcgc gctccaact cagctgtgcc cccagccact gtggaagcct ttgtggaaag 6840
agacagcctc cattttcttc atcctgtgat gatttatgcc aatgtgaaac agggatttta 6900
tcccattctt aatgccactg tcactgccac agttgagcca gagactggag atcctgttac 6960
gctgagactc cttgatgatg gagcaggtgc tgatgttata aaaaatgatg gaatttactc 7020
gaggatattt ttctcctttg ctgcaaattg tagatatagc ttgaaagtgc atgtcaatca 7080
ctctcccagc ataagcacc cagcccactc tattccaggg agtcatgcta tgtatgtacc 7140
aggttacaca gcaaacggta atattcagat gaatgctcca aggaaatcag taggcagaaa 7200
tgaggaggag cgaaagtggg gcttttagccg agtcagctca ggaggctcct ttccagtgtc 7260
gggagttcca gctggcccc accctgatgt gtttccacca tgcaaaatta ttgacctgga 7320
agctgtaaaa gtagaagagg aattgaccct atcttggaac gcacctggag aagactttga 7380
tcagggccag gctacaagct atgaaataag aatgagtaaa agtctacaga atatccaaga 7440
tgactttaac aatgctatatt tagtaaatac atcaaagcga aatcctcagc aagctggcat 7500
caggagagata ttacgtttct caccacaaat ttccacgaat ggacctgaac atcagccaaa 7560
tgagaaaaca catgaaagcc acagaattta tgttgcaata cgagcaatgg ataggaactc 7620
cttacagtct gctgtatcta acattgccca ggcgcctctg ttatttccc ccaattctga 7680
tcctgtacct gccagagatt atottatatt gaaaggagtt ttaacagcaa tgggtttgat 7740
aggaatcatt tgccttatta tagttgtgac acatcatact ttaagcagga aaaagagagc 7800
agacaagaaa gagaatggaa caaaattatt ataatgaatt ctgcagatat ccatcacact 7860
ggcggccgct cgagcaccac caccaccacc actgagatcc ggctgctaac aaagcccga 7920
aggaagctga gttggctgct gccaccgctg agcaataact agcataaccc cttggggcct 7980
ctaaacgggt cttgaggggt tttttgctga aaggaggaac tatatccgga t 8031

```

<210> 255

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 9, 67, 247, 275, 277, 397

<223> n = A,T,C or G

<400> 255

```

gtggccagng actagaaggc gaggcgccgc gggaccatgg cggcggcgcg ggacgagcgg 60
agtccanagg acggagaaga cgaggaagag gaggagcagt tggttctggt ggaattatca 120
ggaattattg attcagactt cctctcaaaa tgtgaaaata aatgcaaggt tttgggcatt 180
gacactgaga ggcccattct gcaagtggac agctgtgtct ttgctgggga gtatgaagac 240
actctangga cctgtgttat atttgaagaa aatgntnaac atgctgatac agaaggcaat 300
aataaaacag tgctaaaata taaatgccat acaatgaaga agctcagcat gacaagaact 360
ctcctgacag agaagaagga aggagaagaa aacatangtg g 401

```

<210> 256

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 7, 37, 51, 79, 96, 98, 103, 104, 107, 116, 167, 181, 183, 194, 206, 276, 303, 307, 308, 310, 323, 332, 341, 353, 374, 376

<223> n = A,T,C or G

<400> 256

```

tggatggnct gggatggga accgcggtg cttccngga ggtttcggca ntggcatccg 60
ggccgggggt cgccggccng gacggggccg gggccnangc cgnnganctc gcggangcaa 120
ggccgaggat aaggagtga tgcccgtcac caacttgggc cgcttgncca aggacatgaa 180
nancagccc ctgnaggaga totatntctt cttccctgcc ccattaagga atcaagagat 240
catttgattt cttcctgggg gcctctctca aggatnaggt ttttgaagat tatgccagt 300
canaaannan acccgttgc ccngtccatc tncaccaac ncttccaagg gcnatTTTTg 360
tttaggcctc attncngggg ggaaccttaa cccaatttgg g

```

401

<210> 257

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 382, 387

<223> n = A,T,C or G

<400> 257

```

atgtatgtaa aacacttcat aaaatgtaaa gggctataac aaatatgtta taaagtgatt 60
ctctcagccc tgagggtatac agaatcattt gcctcagact gctgttggat tttaaaattt 120
ttaaaatata tgctaagtaa tttgctatgt cttctccac actatcaata tgctgcttc 180
taacaggctc cccactttct ttaaatgtgc tgttatgagc tttggacatg agataaccgt 240
gcctgttcag agtgtctaca gtaagagctg gacaaactct ggagggacac agtctttgag 300
acagctcttt tggttgcttt ccacttttct gaaaggttca cagtaacctt ctagataata 360
gaaactccca gttaaagcct angctancaa ttttttttag t

```

401

<210> 258

<211> 401

<212> DNA

<213> Homo sapiens

<400> 258

```

ggagcgctag gtcggtgtac gaccgagatt aggtgtcgtg ccagctccgg gaggcgcgg 60
tgaggggccg ggcccaagct gccgacccga gccgatcgtc aggttcgcca gcgcctcagc 120
tctgtggagg agcagcagta gtcggagggg gcaggatatt agaaatggct actccccagt 180
caattttcat ctttgcaatc tgcatTTTTa tgataacaga attaattctg gcctcaaaaa 240
gtactatga tatcttaggt gtgcaaaaat cggcatcaga gcgccaaatc aagaaggcct 300
ttcacaagtt ggccatgaag taccaccctg acaaaaataa gaccagatg ctgaagcaaa 360
attcagagag attgcagaag catatgaaac actctcagat g

```

401

<210> 259

<211> 401

<212> DNA

<213> Homo sapiens

<400> 259

```

attgggtttg gagggaggat gatgacagag gaatgccctt tggccatcac ggTTTTgatt 60
ctccagaata ttgtgggttt gatcatcaat gcagtcagat taggctgcat tttcatgaaa 120

```


117

```
acagctcagg ctacagaag ggcagaaact ttgattttca gccgccatgc tgtgattgcc 180
gtccgaaatg gcaagctgtg cttcatgttc cgagtgggtg acctgaggaa aagcatgac 240
attagtgcct ctgtgcgcat ccaggtggtc aagaaaacaa ctacacctga aggggaggtg 300
gttctatttc accaactgga cattcctgtt gataaccaa tcgagagcaa taacattttt 360
ctggtggccc ctttgatcat ctgccacgtg attgacaagc g 401
```

<210> 260
<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 7, 9, 19, 41, 63, 73, 106, 111, 113, 116, 119, 156, 158,
162, 187, 247, 288, 289, 290, 292, 298, 299, 300, 340
<223> n = A,T,C or G

```
<400> 260
aggaganang gagggggana tgaatagga tggagagga natagtggat gagcaggga 60
caggagagg aancagaaag gagaggcaag acagggagac acacancaca nangangana 120
caggtggggg ctgggggtggg gcatggagag cctttnangt cncccaggcc accctgctct 180
cgctgggctg ttgaaaccca ctccatggct tctgccact gcagttgggc ccagggtg 240
cttattnctg gaatgcaagt ggctgtggct tggagcctcc cctctggnnn anggaaannn 300
attgctccct tatctgcttg gaatatctga gtttttccan cccggaata aaacacacac 360
aca 363
```

<210> 261
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 114, 152
<223> n = A,T,C or G

```
<400> 261
cggtctccg ccgctctccc ggggtttcgg ggcacttggg tcccacagtc tggctctgct 60
tcaccttccc ctgacctgag tagtcgccat ggcacaggtt ctgagaggca ctgngactga 120
cttccctgga tttgatgagc gggctgatgc anaaactctt cggaaggcta tgaaaggctt 180
gggcacagat gaggagagca tctgactct gttgacatcc cgaagtaatg ctgagcgcca 240
ggaaatctct gcagcttita agactctgtt tggcagggat cttctggatg acctgaaatc 300
agaactaact ggaaaatttg aaaaattaat tgtggctctg atgaaaccct ctcggttita 360
tgatgcttat gaactgaaac atgccttgaa gggagctgga a 401
```

<210> 262
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 7, 26, 258, 305, 358, 373, 374, 378
<223> n = A,T,C or G

```
<400> 262
agtctanaac atttctaata ttttngctt tcatatatca aaggagatta tgtgaaacta 60
tttttaaata ctgtaaagtg acatatagtt ataagatata tttctgtaca gtagagaaag 120
```

```
agtttataac atgaagaata ttgtaccatt atacattttc attctcgatc tcataagaaa 180
ttcaaaagaa taatgataga ggtgaaaata tgtttacttt ctctaaatca agcctagttg 240
tcaactcaaa aattatgntg catagtttta ttttgaattt aggttttggg actacttttt 300
tccancttca atgagaaaat aaaatctaca actcaggagt tactacagaa gttctaanta 360
tttttttgct aannagcnaa aaatataaac atatgaaaat g 401
```

<210> 263

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 232, 290, 304, 326, 383

<223> n = A,T,C or G

<400> 263

```
ctgtccgacc aagagaggcc ggccgagccc gaggcttggg cttttgcttt ctggcggagg 60
gatctgcggc ggttttaggag gcggcgctga tcctgggagg aagaggcagc tacggcggcg 120
gcggcgggtg cggctagggc ggcgcgcaat aaaggggccc ccgccgggtg atgcggtgac 180
cactgcggca ggcccaggag ctgagtgggc cccggccctc agcccgctcc gncggacccg 240
ctttcctcaa ctctccatct tctcctgccg accgagatcg ccgaggcggn ctcaggctcc 300
ctanccctt ccccgctcct tcccncccc cgtccccgcc ccggggggccg ccgccaccgc 360
cctcccacca tggctctgaa ganaatccac aaggaattga a 401
```

<210> 264

<211> 401

<212> DNA

<213> Homo sapiens

<400> 264

```
aacaccagcc actccaggac ccctgaaggc ctctaccagg tcaccagtgt tctgcgccta 60
aagccacccc ctggcagaaa cttcagctgt gtgttctgga atactcacgt gagggaaact 120
actttggcca gcattgacct tcaaagtcag atggaaccca ggacccatcc aacttggctg 180
cttcacattt tcatcccctc ctgcatcatt gctttcattt tcatagccac agtgatagcc 240
ctaagaaaac aactctgtca aaagctgtat tcttcaaaag acacaacaaa aagacctgtc 300
accacaacaa agaggggaagt gaacagtgtc gtgaatctga acctgtggtc ttgggagcca 360
gggtgacctg atatgacatc taaagaagct tctggactct g 401
```

<210> 265

<211> 271

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 59

<223> n = A,T,C or G

<400> 265

```
gccacttcct gtggacatgg gcagagcgct gctgccagtt cctggtagcc ttgaccacna 60
cgctgggggg tctttgtgat ggtcatgggt ctcatttgca cttgggggtg tgggattcaa 120
gttagaagtt tctagatctg gccgggcgca gtggctcaca cctgtaatcc cagcacttta 180
ggaggctgag gcaggcggt catgaggtca ggagatcgag accgtcctgg ctaacacagt 240
gaaaccccg tctactaaa aatacaaaaa a 271
```

<210> 266

<211> 401

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 45
<223> n = A,T,C or G

<400> 266
attcataaat ttagctgaaa gatactgatt caatttgtat acanggaata taaatgagac 60
gacagcaaaa ttttcatgaa atgtaaaata tttttatagt ttgttcatac tatatgaggt 120
tctatttttaa atgactttct ggatttttaa aaatttcttt aaatacaatc atttttgtaa 180
tattttatttt atgcttatga tctagataat tgcagaatat cattttatct gactctgtct 240
tcataagaga gctgtggccg aattttgaac atctgttata gggagtgtac aaattagaag 300
gcaatgtgga aaaacaattc tgggaaagat ttctttatat gaagtccttg ccactagcca 360
gccatcctaa ttgatgaaag ttatctgttc acaggcctgc a 401

<210> 267
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 116, 247, 277, 296, 307, 313, 322, 323, 336, 342, 355, 365,
377, 378, 397
<223> n = A,T,C or G

<400> 267
gaagaggcat cacctgatcc cggagacctt tggagttaag aggcggcgga agcgagggcc 60
tgtggagtgc gatcctcttc ggggtgagcc agggtcggcg cgcgcggtcg tctcanaact 120
catgcaagtgc ttcccgcgag gcctgtttga ggacgcgctg ccgccatcg tgctgaggag 180
ccaggtgtac agccttgtgc ctgacaggac cgtggccgac cggcagctga aggagcttca 240
agagcanggg gagacaaaat cgtccagctg ggcttcnact tggatgcca tggaanttat 300
tctttcnctt ganggactta onngggaccc aagaancct tncaaggggc ccttngtggg 360
tggnccccga aaccccnnta tttgcccttg ggggggncca a 401

<210> 268
<211> 223
<212> DNA
<213> Homo sapiens

<400> 268
tcgccatgtt ggccaggctg gtcttgaact cctgacttta agtgateccac ccgcctcaac 60
ctcccaaagt gctgggatta caggtgtgag ccaccgcgc tggcctgata catactttta 120
gaatcaagta gtcacgcaact ttttctgttc atttttctaa aaagtaaata tacaatgtt 180
ttgttttttg ttttttttgt ttgtttgttt ctgttttttt ttt 223

<210> 269
<211> 401
<212> DNA
<213> Homo sapiens

<400> 269
actatgtaaa ccacattgta ctttttttta ctttggcaac aaatatttat acatacaaga 60
tgctagtcca tttgaatatt tctcccaact tatccaagga tctccagctc taacaaaatg 120
gtttattttt atttaaatgt caatagttgt tttttaaaat ccaaatacaga ggtgcaggcc 180
accagtaaaa tgccgtctat caggttttgt gccttaagag actacagagt caaagtcctat 240

```

ttttaaagga gtaggacaaa gtgtgcacag gtttttgttg ttgtttttat tgccccaaa 300
attacatggt aatttccatt tatatcaggg attctattta cttgaagact gtgaagttgc 360
cattttgtct cattgttttc tttgacataa ctaggatcca t 401

```

<210> 270

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 240, 382

<223> n = A,T,C or G

<400> 270

```

tggctgttga ttcacctcag cactgcttgg tatctgcacc ctacctctct ttagaggctg 60
ccttgtcaac tgaaaaatgc acctgacttc gagcaagact ctttccttag gttctggatc 120
tgtttgagcc ccatggcact gagctggaat ctgaggggtct tgttccaagg atgtgatgat 180
gtggggagaat gttctttgaa agagcagaaa tccagtctgc atggaaacag cctgtagagn 240
agaagtttcc agtgataagt gttcactgtt ctaaggaggt acaccacagc tacctgaatt 300
ttcccaaaat gagtgcttct gtgcgttaca actggccttt gtacttgact gtgatgactt 360
tgttttttct tttcaattct anatgaacat gggaaaaaat g 401

```

<210> 271

<211> 329

<212> DNA

<213> Homo sapiens

<400> 271

```

ccacagcctc caagtcaggt ggggtggagt cccagagctg cacagggttt ggcccaagtt 60
tctaagggag gcaattcttc ccctcgcca tcagtgccag cccctgctgg ctgggtgcctg 120
agccctcag acagcccctt gcccgcagg cctgccttct cagggacttc tgcggggcct 180
gaggcaagcc atggagttag acccaggagc cggacacttc tcaggaaatg gcttttcca 240
acccccagcc cccaccgggt ggttcttctt gttctgtgac tgtgtatagt gccaccacag 300
cttatggcat ctcataggag acaaaaaaa 329

```

<210> 272

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 1, 7, 12, 21, 61, 62, 66, 72, 78, 88, 90, 92, 98, 117, 119, 128, 130, 134, 142, 144, 151, 159, 162, 164, 168, 169, 177, 184, 185, 188, 194, 202, 204, 209, 213, 218, 223, 231, 260, 272, 299, 300, 306, 321, 322, 323, 331, 335, 336, 338

<223> n = A,T,C or G

<221> misc_feature

<222> 341, 342, 343, 345, 346, 351, 358, 360, 362, 363, 387, 390, 392

<223> n = A,T,C or G

<400> 272

```

nggctgntaa cntcggaggt nacttcctgg actatcctgg agacccctc cgcttccacg 60
nncatnatat cnetcatngc tgggccntn angacacnat cccactccaa cacctgngng 120
atgctggnnc cctnggaacc ancntcagaa ngaccctgnt cntntgtntt ccgcaantcg 180

```

121

```

aagnnaangc gggntacacc tncntgcant ggnccacnct gcngggaact ntacacacct 240
acgggatgtg gctgcgccan gagccaagag cntttctgga tgattcccca gcctcttggn 300
agggantcta caacattgct nnntaccttt ntcnncngc nnntnntgga ntacaggngn 360
tnntaacact acatcttttt tactgcncn tnccttggtg g 401

```

<210> 273

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 399

<223> n = A,T,C or G

<400> 273

```

cagcaccatg aagatcaaga tcatcgccac ccagagcgcg aagtactcgg tgtggatcgg 60
tggtccatc ctggcctcac tgtccacctt ccagcagatg tggattagca agcaggagta 120
cgacgagtcg ggccccctcca tcgtccaccg caaatgcttc taaacggact cagcagatgc 180
gtagcatttg ctgcatgggt taattgagaa tagaaatttg cccctggcaa atgcacacac 240
ctcatgctag cctcacgaaa ctggaataag ccttcgaaaa gaaattgtcc ttgaagcttg 300
tatctgatat cagcactgga ttgtagaact tgttgctgat ttgaccttg tattgaagtt 360
aactgttccc cttggtatta acgtgtcagg gctgagtnt c 401

```

<210> 274

<211> 401

<212> DNA

<213> Homo sapiens

<400> 274

```

ccaccacac ccaccgcgc ctcgttcgcc tcttctccgg gagccagtcc gcgccaccgc 60
cgccgccag gccatcgcca ccctccgcag ccatgtccac caggtcctg tcctcgctct 120
cctaccgcag gatgttcggc ggcccgggca ccgcgagccg gccgagctcc agccggagct 180
acgtgactac gtccaccgc acctacagcc tgggcagcgc gctgcgcccc agcaccagcc 240
gcagcctcta cgcctcgcc ccgggcggcg tgtatgccac gcgctcctct gccgtgcgcc 300
tgccgagcag cgtgcccggg gtgcggctcc tgcaggactc ggtggacttc tcgctggccg 360
acgccatcaa caccgagttc aagaacaccc gcaccaacga g 401

```

<210> 275

<211> 401

<212> DNA

<213> Homo sapiens

<400> 275

```

ccacttcac cactttgtgg agcagtgcct tcagcgcaac ccggatgcca ggtatccctg 60
ctggcctggg cctgggcttc gggagagcag aggggtgctca ggagggtgta gccagggtgt 120
gaagggactt acctccaaa ggttctgcag gggaaatctg agctacacac aggagggatc 180
agctcctggg tgtgtcagag gccagcctgg ggagctctgg ccaactgcttc ccatgagctg 240
aggagagagg agaggggacc cgaggctgag gcataagtgg caggatttcg ggaagctggg 300
gacacggcag tgatgctgcg gtctctcttc ccctttccct ccaggcccag tgccagcacc 360
ctctgtaacc actctttctt caagcagatc aagcgacgtg c 401

```

<210> 276

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> 11
<223> n = A,T,C or G

<400> 276
tctgatattg ntacccttga gccacctaag ttagaagaaa ttggaaatca agaagttgtc 60
attgttgaag aagcacagag ttcagaagac tttaacatgg gctcttcctc tagcagccag 120
tatactttct gtcagccaga aactgtattt tcatctcagc ctagtgatga tgaatcaagt 180
agtgatgaaa ccagtaatca gcccagtcct gccttttagac gacgccgtgc taggaagaag 240
accgtttctg cttcagaatc tgaagaccgg ctagtgtgtg aacaagaaac tgaaccttct 300
aaggagttga gtaaactgca gttcagtagt ggtctcaata agtgtgttat acttgctttg 360
gtgattgcaa tcagcatggg atttgccat ttctatggca c 401

<210> 277
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 227, 333
<223> n = A,T,C or G

<400> 277
aactttggca acatatctca gcaaaaacta cagctatggt attcatgcc aataaaaagc 60
tgtgcagagg agtggctgca atgaggtcac aacgggtgtg gatgtaaaag agatcttcaa 120
gtcctcatca cccatccctc gaactcaagt cccgctcatt acaaattctt cttgccagtg 180
tccacacatc ctgccccatc aagatgttct catcatgtgt tacgagnggc gctcaaggat 240
gatgcttctt gaaaattgct tagttgaaaa atggagagat cagcttagta aaagatccat 300
acagtgggaa gagaggctgc aggaacagcg ganaacagtt caggacaaga agaaaacagc 360
cgggcgccacc agtcgtagta atcccccaa accaaagga a 401

<210> 278
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 322, 354
<223> n = A,T,C or G

<400> 278
aatgagtgtg agaccacaaa tgaatgccgg gaggatgaaa tgtgttggaa ttatcatggc 60
ggcttccggt gttatccacg aaatccttgt caagatccct acattctaac accagagaac 120
cgatgtgttt gcccagtcct aaatgccatg tgccgagaac tgccccagtc aatagtctac 180
aaatacatga gcatccgata tgataggtct gtgccatcag acatcttcca gatacaggcc 240
acaactatct atgccaacac catcaatact ttctcgatta aatctggaaa tgaaaatgga 300
gagtctacct acgacaacaa anccctgtaa gtgcaatgct tgtgctcgtg aagncattat 360
caggaccaag agaacatatc gtggacctgg agatgctgac a 401

<210> 279
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> 30, 35, 81, 88, 180, 212, 378, 384, 391

<223> n = A,T,C or G

<400> 279

```

aaattattgc ctctgataca tacctaagtn aacanaacat taatacctaa gtaaacataa 60
cattacttgg agggttgcag nttctaantg aaactgtatt tgaaactttt aagtatactt 120
taggaaacaa gcatgaacgg cagtctagaa taccagaaac atctacttgg gtagcttggg 180
gccattatcc tgtggaatct gatatgtctg gnagcatgtc attgatggga catgaagaca 240
tctttgaaa tgatgagatt atttcctgtg ttaaaaaaaa aaaaaatctt aaattcctac 300
aatgtgaaac tgaaactaat aattttgatc ctgatgtatg ggacagcgta tctgtaccag 360
gctctaaata acaaaagnta gggngacaag nacatgttcc t 401

```

<210> 280

<211> 326

<212> DNA

<213> Homo sapiens

<400> 280

```

gaagtggaat tgtataattc aattcgataa ttgatctcat gggctttccc tggaggaaaag 60
gttttttttt ttgttttttt tttaagaact tgaaacttgt aaactgagat gtctgtagct 120
tttttgccca tctgtagtgt atgtgaagat ttcaaaacct gagagcactt tttctttgtt 180
tagaattatg agaaaggcac tagatgactt taggatttgc atttttccct ttattgcctc 240
atttcttgtg acgccttgtt ggggagggaa atctgtttat tttttcctac aaataaaaaag 300
ctaagattct atatcgcaaa aaaaaa 326

```

<210> 281

<211> 374

<212> DNA

<213> Homo sapiens

<400> 281

```

caacgcgttt gcaaatattc ccctggtagc ctacttcctt acccccgaat attggtaaga 60
tcgagcaatg gcttcaggac atgggttctc ttctcctgtg atcattcaag tgctcactgc 120
atgaagactg gcttgtctca gtgtttcaac ctcaccaggg ctgtctcttg gtccacacct 180
cgctccctgt tagtgccgta tgacagcccc catcaaata ccttggccaa gtcacggttt 240
ctctgtggtc aagggttggtt ggctgattgg tggaaagtag ggtggaccaa aggaggccac 300
gtgagcagtc agcaccagtt ctgcaccagc agcgcctccg tcctagtggg tggttcctgtt 360
tctcctggcc ctgg 374

```

<210> 282

<211> 404

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> 26, 27, 51, 137, 180, 222

<223> n = A,T,C or G

<400> 282

```

agtgtggtgg aattcccgcg tcctanncgc cgactcacac aaggcagagt ngccatggag 60
aaaattccag tgtcagcatt cttgctcctt gtggccctct cctacactct ggccagagat 120
accacagtca aacctgnagc caaaaaggac acaaaggact ctcgacccaa actgccccan 180
accctctcca gaggttgggg tgaccaactc atctggactc anacatatga agaagctcta 240
tataaatcca agacaagcaa caaaccttg atgattatc atcacttgga tgagtgccca 300
cacagtcaag ctttaagaa agtgtttgc t gaaaataaag aaatccagaa attggcagag 360
cagtttgtcc tcctcaatct ggtttatgaa acaactgaca aaca 404

```

<210> 283
<211> 184
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 26
<223> n = A,T,C or G

<400> 283
agtgtggtgg aattcacttg cttaanttgt gggcaaaaga gaaaaagaag gattgatcag 60
agcattgtgc aatacagttt cattaactcc tccctcgct cccccaaaaa ttggaatttt 120
tttttcaaca ctcttacacc tggtatggaa aatgtcaacc ttgtaagaa aacaaaaata 180
aaaa
184

<210> 284
<211> 421
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 147, 149
<223> n = A,T,C or G

<400> 284
ctattaatcc tgccacaata tttttaatta cgtacaaaga tctgacatgt caccagggga 60
cccatttcac ccactgctct gtttgccgc cagtcttttg tctctctctt cagcaatggt 120
gaggcggata ccctttcctc ggggaanana aatccatggt ttgttgccct tgccaataac 180
aaaaatggtg gaaagtcgag tggcaaagct gttgccattg gcatctttca cgtgaaccac 240
gtcaaaagat ccagggtgcc tctctctggt ggtgatcaca ccaattcttc ctagggttagc 300
acctccagtc accatacaca ggttaccagt gtcgaacttg atgaaatcag taatcttgcc 360
agtctctaaa tcaatctgaa tggatcatt caccttgatg aggggatcgg ggtagcggat 420
g
421

<210> 285
<211> 361
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 34, 188
<223> n = A,T,C or G

<400> 285
ctgggtggta actctttatt tcattgtccg gaanaaagat gggagtggga acagggtgga 60
cactgtgcag gcttcagctt ccactccggg caggattcag gctatctggg accgcaggga 120
ctgccagggtg cacagccctg gctcccgagg caggcaggca aggtgacggg actggaagcc 180
cttttcanag ccttgaggga gctgggtccg ccacaagcaa tgagtgccac tctgcagttt 240
gcaggggatg gataaacagg gaaacactgt gcattcctca cagccaacag ttaggtctt 300
ggtgaagccc cggcgctgag ctaagctcag gctgttccag ggagccacga aactgcaggt 360
a
361

<210> 286
<211> 336
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 40, 68, 75, 127, 262

<223> n = A,T,C or G

<400> 286

```

tttgagtggc agcgccttta tttgtggggg ccttcaaggn agggtcgtgg ggggcagcgg 60
ggaggaanag ccganaaact gtgtgaccgg ggcctcaggt ggtgggcatt gggggctcct 120
cttgcanaatg ccatttggca tcaccggtgc agccattggt ggcagcgggt accggtcctt 180
tcttgttcaa catagggtag gtggcagcca cgggtccaac tcgcttgagg ctgggacctg 240
ggcgctccat tttgtgttcc angagcatgt ggttctgtgg cgggagcccc acgcaggccc 300
tgaggatggt ctcgatgcag ctgcgctggc ggaaaa 336

```

<210> 287

<211> 301

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 15, 33, 44, 53, 76, 83, 107, 117, 154, 166, 192, 194, 207,
215, 241, 246

<223> n = A,T,C or G

<400> 287

```

tgggtaccaa attnttttat ttgaaggaat ggnacaaatc aaanaactta agnggatggt 60
ttgttacaac ttatanaaaa ggnaaaggaa accccaacat gcatgcncctg ccttgngnac 120
cagggaagtc accccacggc tatggggaaa ttancccgag gcttancttt cattatcact 180
gtctcccagg gngngcttgt caaaaanata ttccnccaag ccaaattcgg gcgctcccat 240
nttgcnaag ttggtcacgt ggtcacccaa ttctttgatg gctttcacct gctcattcag 300
g 301

```

<210> 288

<211> 358

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 39, 143, 226

<223> n = A,T,C or G

<400> 288

```

aagtttttaa actttttatt tgcatattaa aaaaattgng cattccaata attaaaatca 60
tttgaacaaa aaaaaaaatg gcactctgat taaactgcat tacagcctgc aggacacctt 120
gggccagctt ggttttactc tanatttcac tgtcgtccca ccccaacttc tccacccac 180
ttcttccttc accaacaatgc aagttctttc ctccctgcc agccanata atagacagat 240
gggaaaggca ggcgcggcct tcgttgtcag tagttctttg atgtgaaagg ggcagcacag 300
tcatttaaac ttgatccaac ctctttgcat cttacaaagt taaacagcta aaagaagt 358

```

<210> 289

<211> 462

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature
<222> 87, 141, 182, 220, 269, 327
<223> n = A,T,C or G

<400> 289
ggcatcagaa atgctgttta tttctctgct gctcccaagc tggctggcct ttgcagagga 60
gcagacaaca gatgcatagt tgggganaaa gggaggacag gttccaggat agaggggtgca 120
ggctgaggga ggaagggtaa naggaaggaa ggccatcctg gatccccaca tttcagtctc 180
anatgaggac aaagggactc ccaagccccc aaatcatcan aaaacaccaa ggagcaggag 240
gagcttgagc aggcccccagg gagcctcana gccataccag ccaactgtcta cttcccatcc 300
tcctctccca ttccctgtct gcttcanacc acctcccagc taagcccag ctcattccc 360
ccaatcctgg cccttgccag cttgacagtc acagtgcctg gaattccacc actgaggctt 420
ctccaggttg gattaggacg tcgccctgtt agcatgctgc cc 462

<210> 290
<211> 481
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 44, 57, 122, 158, 304, 325, 352, 405
<223> n = A,T,C or G

<400> 290
tactttccta aactttatta aagaaaaaag caataagcaa tggnggtaaa tctctanaac 60
atacccaatt ttctgggctt cctcccccga gaatgtgaca ttttgatttc caaacatgcc 120
anaagtgtat gggtcccaac tgtactaaag taggtganaa gctgaagtcc tcaagtgttc 180
atcttccaac ttttcccagt ctgtggtctg tctttggatc agcaataatt gcctgaacag 240
ctactatggc ttctgtgatt tttgtctgta gctctctgag ctctctatg tgcagcaatc 300
gcanaatttg agcagcttca ttaanaactg catctcctgt gtcaaaaacca anaatatgtt 360
tgtctaaagc aacaggttaag ccctcttttg tttgatttgc cttancaact gcatcctgtg 420
tcaggcgctc ctgaacaaaa atccgaattg ccttaagcat taccaggtta tcatcatgac 480
g 481

<210> 291
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 79, 166, 187, 208, 219, 315
<223> n = A,T,C or G

<400> 291
tcatagtaat gtaaaacat ttgtttaatt ctaaatcaaa tcactttcac aacagtgaag 60
attagtgact gggttaaggng tgccactgta catatcatca ttttctgact ggggtcagga 120
cctggctcta gtccacaagg gtggcaggag gaggggtggag gctaanaaca cagaaaacac 180
acaaaanaaa ggaaagctgc cttggcanaa ggatgaggng gtgagcttgc cgaaggatgg 240
tgggaagggg gctccctgtt ggggcccagc caggagtccc aagtcagctc tctgcctta 300
cttagctcct ggcanagggt gagtggggac ctacgagggt caaaatcaaa tggcatttgg 360
ccagcctggc ttactaaca g 381

<210> 292
<211> 371
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 32, 55, 72, 151, 189, 292
<223> n = A,T,C or G

<400> 292
gaaaaaataa tccgtttaat tgaaaaacct gnaggatact attccactcc cccanattgag 60
gaggctgagg anaccaaacc cctacatcac ctctgtagca cttctgatac tcttcacgag 120
gcagcaggca aagacaattc ccaaaacctc nacaaaagca attccaaggg ctgctgcagc 180
taccaccanc acattttttcc tcagccagcc cccaatcttc tccacacagc cctccttatg 240
gatcgcttc tcgttgaaat taatcccaca gccacagta acattaatgc ancaggagtc 300
ggggactcgg ttcttcgaca tggaagggat tttctccaa tctgtgtagt tagcagcccc 360
acagcactta a 371

<210> 293
<211> 361
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 75, 196, 222
<223> n = A,T,C or G

<400> 293
gatttaaaag aaaacacttt attgttcagc aattaaaagt tagccaaata tgtatttttc 60
tcataatttt attgngatgt tatcaacatc aagtaaaatg ctcatthttca tcatthgctt 120
ctgttcatgt tttcttgaac acgtcttcaa ttttccttcc aaaatgctgc atgccacact 180
tgaggtaacg aagcanaagt atttttaaac atgacagcta anaacattca tctacagcaa 240
cctatatgct caatacatgc cgcgtgatcc tagtagtttt ttcacaacct tctacaagtt 300
tttggaaac atctgttatg atgactttca tacaccttca cctcaaaggc tttcttgcc 360
c 361

<210> 294
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> 26, 77, 96, 150, 203, 252, 254, 264, 276
<223> n = A,T,C or G

<400> 294
tatttttaaag ttttaattatg attcanaaaa aatcgagcga ataactttct ctgaaaaaat 60
atattgactc tgtatanacc acagttattg gggganaagg gctggtagg taaattatcc 120
tattttttat tctgaaaatg atattaatan aaagtcccg ttcagctctg attataaaga 180
tacatatgcc caaaatggct ganaataaat acaacaggaa atgcaaaagc tgtaaagcta 240
agggcatgca ananaaaatc tcanaatacc caaagnggca acaaggaacg tttggctgga 300
atttgaaagt atttcagtc tctttgtctt tggctccatg tttcaggatg cgtgtgaact 360
cgatgtaatt gaaattcccc tttttatcaa t 391

<210> 295
<211> 343
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 145, 174, 205, 232
<223> n = A,T,C or G

<400> 295
ttcttttgtt ttattgataa cagaaactgt gcataattac agatttgatg aggaatctgc 60
aaataataaa gaatgtgtct actgccagca aaatacaatt attccatgcc ctctcaacat 120
acaaatatag agttcttcac accanatggc tctggtgtaa caaagccatt ttanatgttt 180
aattgtgctt ctacaaaacc ttcanagcat gaggtagttt cttttaccta cnatattttc 240
cacatttcca ttattacact tttagtgagc taaaatcctt ttaacatagc ctgcggatga 300
tctttcaciaa aagccaagcc tcatttacaa agggttttatt tct 343

<210> 296
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 96, 98, 106, 185
<223> n = A,T,C or G

<400> 296
ttcttgata ttggttgttt ttgtgaaaaa gtttttgttt ttcttctcag tcaactgaat 60
tatttctcta ctttgcoctc ctgatgccca catgananaa cttaanataa tttctaacag 120
cttcactttt ggaaaaaaa aaaacctgtt ttcctcatgg aaccccagga gttgaaagt 180
gatanatcgc tctcaaaatc taaggctctg ttcagcttta cattatgtta cctgacgttt 240
t 241

<210> 297
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 12, 130
<223> n = A,T,C or G

<400> 297
gttgtggctg anaatgctgg agatgctcag ttctctccct cacaaggtag gccacaaatt 60
cttggtggtg ccctcacatc tggggtcttc aggcaccagc catgcctgcc gaggagtgtc 120
gtcaggacan accatgtccg tgctaggccc aggcacagcc caaccactcc tcatccaagt 180
ctctcccagg tttctggtcc cgatgggcaa ggatgacccc tccagtggct ggtacccac 240
catccacta ccctcacat gctctcactc tccatcaggt ccccaatcct ggcttccctc 300
ttcacgaact ctcaaagaaa aggaaggata aaacctaat aaaccagaca gaagcagctc 360
tggaaaagta caaaaagaca gccagaggtg t 391

<210> 298
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 14, 30, 76, 116, 201, 288, 301
<223> n = A,T,C or G

<400> 298
 caagccaaac tgtntccagc tttatttaaan atactttcca taaacaatca tgggtatttca 60
 ggcaggacat gggcanacaa tcgttaacag tatacaacaa ctttcaaact cccttnttca 120
 atggactacc aaaaatcaaa aagccactat aaaacccaat gaagtcttca tctgatgctc 180
 tgaacagggg aagttttaaag ngagggttgga catttcacat ttagcatggt gtttaacaac 240
 ttttcacaag ccgaccctga ctttcaggaa gtgaaatgaa aatggcanaa tttatctgaa 300
 natccacaat ctaaaaatgg a 321

<210> 299
 <211> 401
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 104, 268, 347
 <223> n = A,T,C or G

<400> 299
 tatcataaag agtgttgaag tttattttatt atagcaccat tgagacattt tgaaattgga 60
 attggtaaaa aaataaaaaca aaaagcattt gaattgtatt tggnggaaca gcaaaaaaag 120
 agaagtatca tttttctttg tcaaattata ctgtttccaa acattttgga aataaataac 180
 tggaaatttg tcggtcactt gcactggttg acaagattag aacaagagga acacatatgg 240
 agttaaattt tttttgttgg gatttcanat agagtttggg ttataaaaag caaacagggc 300
 caacgtccac accaaattct tgatcaggac caccaatgtc atagggngca atatctacaa 360
 taggtagtct cacagccttg cgtgttcgat attcaaagac t 401

<210> 300
 <211> 188
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 48
 <223> n = A,T,C or G

<400> 300
 tgaatgcttt gtcattattaa gaaagttaaa gtgcaataat gtttgaanac aataagtggg 60
 ggtgtatctt gtttctaata agataaacct ttttgtctt gctttatctt attagggagt 120
 tgtatgtcag tgtataaaac atactgtgtg gtataacagg cttaataaat tctttaaaag 180
 gaaaaaaa 188

<210> 301
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 301
 aagattttgt tttattttat tatggctaga aagacactgt tatagccaaa atcggcaatg 60
 acactaaaga aatcctctgt gcttttcaat atgcaaatat atttcttcca agagttgcc 120
 tgggtgtgact tcaagagttc atgttaactt cttttctgga aacttccttt tcttagttgt 180
 tgtattcttg aagagcctgg gccatgaaga gcttgccctaa gttttgggca gtgaactcct 240
 tgatgttctg gcagtaagtg tttatctggc ctgcaatgag cagcgagtcc a 291

<210> 302
 <211> 341

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 25
<223> n = A,T,C or G

<400> 302
tgattttttca taatttttatt aaatnatcac tgggaaaact aatggttcgc gtatcacaca 60
attacactac aatctgatag gagtggtata accagccaat ggaatccagg taaagtacaa 120
aaacgccacc ttttattgtc ctgtcttatt tctcgggaag gaggggttcta ctttacacat 180
ttcatgagcc agcagtggtc ttgagttaca atgtgtaggt tccttgtggt tatagctgca 240
gaagaagcca tcaaattctt gaggacttga catctctcgg aaagaagcaa actagtggat 300
cccccggtgc gcaggaattc gatatcaagc ttatcgatac c 341

<210> 303
<211> 361
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 15, 27, 92, 124, 127, 183, 198, 244, 320
<223> n = A,T,C or G

<400> 303
tgcagacagt aaatnaattt tatttgngtt cacagaacat actaggcgat ctgcacagtc 60
gctccgtgac agcccaccaa cccccaaccc tntacctcgc agccacccta aaggcgactt 120
caanaanatg gaaggatctc acggatctca ttctaatgg tccgcggaag tctcacacag 180
tanacagacg gagttganat gctggaggat gcagtcacct cctaaactta cgaccaccca 240
ccanacttca tcccagccgg gacgtcctcc cccacccgag tcctcccat ttcttctcct 300
actttgccgc agttccaggn gtctgtcttc caccagtccc acaaagctca ataaatacca 360
a 361

<210> 304
<211> 301
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 23, 104, 192
<223> n = A,T,C or G

<400> 304
ctcttttaca cagcctttat ttncggccct tgatcctgct cggatgctgg tggaggccct 60
tagctccgcc cgccaggctc tgtgccgctt ccccgaggc gcanattcat gaacacggtg 120
ctcaggggct tgaggccgta ctccccagc gggagctggt cctccagggg cttcccctcg 180
aaggtcagcc anaacaggtc gtctgcaca cctccagcc cgctcacttg ctgcttcagg 240
tgggccacgg tctgcgtcag cgcacctcg taggtgctgc tgcggccctt gttattcttc 300
a 301

<210> 305
<211> 331
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature

<222> 3, 36, 60, 193, 223

<223> n = A,T,C or G

<400> 305

```

ganaggctag taacatcagt tttattgggt tgggngggca accatagcct ggctgggggn 60
ggggctggcc ctcacaggtt gttgagttcc agcagggtct ggtccaaggt ctggtgaatc 120
tcgacgttct cctccttggc actggccaag gtctcttcta ggtcatcgat ggttttctcc 180
aactttgcca canacctctc ggcaaactct gctcgggtct cancctcctt cagcttctcc 240
tccaacagtt tgatctcctc ttcataattt tcttctttgg gggaatactc ctcctctgag 300
gccatcaggg acttgagggc ctggtccatg g

```

<210> 306

<211> 457

<212> DNA

<213> Homo sapiens

<400> 306

```

aatatgtaaa ggtaataaact tttattatat taaagacaat gcaaacgaaa aacagaattg 60
agcagtgcaa aatttaaagg actgttttgt tctcaaagtt gcaagtttca aagccaaaag 120
aattatatgt atcaaatata taagtaaaaa aaagtttagac ttccaagcct gtaatcccag 180
cactttggga ggctgaggca ggtggatcac taacattaaa aagacaacat tagattttgt 240
cgatttatag caattttata aatatataac tttgtcactt ggatcctgaa gcaaaataat 300
aaagtgaatt tgggattttt gtacttggtt aaaagtttaa caccctaaat tcacaactag 360
tggatcccc gggtgcagg aattcgatat caagcttatc gataccgtcg acctcgaggg 420
ggggcccggt acccaattcg ccctatagtg agtcgta

```

<210> 307

<211> 491

<212> DNA

<213> Homo sapiens

<400> 307

```

gtgcttgga ggaacccggc gctcgttccc cccccggcc ggccgcccac agccagccct 60
ccgtcacctc ttcaccgcac cctcggactg cccaaggcc cccgcccgcg ctccagcgcc 120
gcgagccac cgccgcccgc gccgcctctc cttagtcgcc gccatgacga ccgcgtccac 180
ctcgaggtg cgccagaact accaccagga ctgagaggcc gccatcaacc gccagatcaa 240
cctggagctc tacgcctcct acgtttacct gtccatgtct tactactttg accgcatga 300
tgtggccttg aagaactttg ccaaatactt tcttcaccaa tctcatgagg agaggaaca 360
tgctgagaaa ctgatgaagc tgcagaacca acgaggtggc cgaatcttcc ttcaggatat 420
caagaaacca gactgtgatg actgggagag cgggctgaat gcaatggagt gtgcattaca 480
tttggaaaaa a

```

<210> 308

<211> 421

<212> DNA

<213> Homo sapiens

<400> 308

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ctcagcgctt cttctttctt ggtttgatcc tgactgctgt catggcgtgc cctctggaga 60
aggccctgga tgtgatggtg tccaccttcc acaagtactc gggcaaagag ggtgacaagt 120
tcaagctcaa caagtcagaa ctaaaggagc tgctgaccgc ggagctgcc agcttcttgg 180
ggaaaaggac agatgaagct gctttccaga agctgatgag caacttgga agcaacaggg 240
acaacgaggt ggacttccaa gagtactgtg tcttcctgtc ctgcatcgcc atgatgtgta 300
acgaattctt tgaaggcttc ccagataagc agcccaggaa gaaatgaaaa ctccctctgat 360
gtggttgagg ggtctgccag ctggggccct ccctgtcgcc agtgggcact ttttttttc 420
c

```

<210> 309
<211> 321
<212> DNA
<213> Homo sapiens

<400> 309
accaaattggc ggatgacgcc ggtgcagcgg gggggcccgg ggccctggt ggccctggga 60
tggggaaccg cgggtggcttc cgcggagggt tgggcagtgg catccggggc cggggtcgcg 120
gccgtggacg gggccggggc cgaggccgcg gagctcgcgg aggcaaggcc gaggataagg 180
agtggatgcc cgtcaccaag ttgggccgct tggtaagga catgaagatc aagtccttg 240
aggagatcta tctcttctcc ctgccatta agaatcaga gatcattgat ttcttctctg 300
gggctctctc caaggatgag g 321

<210> 310
<211> 381
<212> DNA
<213> Homo sapiens

<400> 310
ttaaccagcc atattggctc aataaatagc ttcgtaagg agttaatttc cttctagaaa 60
tcagtgccta ttttctctgg aaactcaatt ttaaatagtc caattccatc tgaagccaag 120
ctgttgtcat tttcattcgg tgacattctc tcccatgaca ccagaaggc gcagaagaac 180
cacatttttc atttatagat gtttgcaccc tttgtattaa aattattttg aaggggttgc 240
ctcattggat ggcttttttt ttttctctcc agggagaagg ggagaaatgt acttggaat 300
taatgtatgt ttacatctct ttgcaaattc ctgtacatag agatatattt ttaagtgtg 360
aatgtaacaa catactgtga a 381

<210> 311
<211> 538
<212> DNA
<213> Homo sapiens

<400> 311
tttgaattta caccaagaac ttctcaataa aagaaaatca tgaatgctcc acaatttcaa 60
cataccacaa gagaagttaa tttcttaaca ttgtgttcta tgattatttg taagaccttc 120
accaagttct gatattcttt aaagacatag ttcaaaattg cttttgaaaa tctgtattct 180
tgaaaatata cttgttgtgt attaggtttt taaataccag cttaaaggatt acctcactga 240
gtcatcagta ccctcctatt cagctcccca agatgatgtg tttttgctta ccctaagaga 300
ggtttttctt ttatttttag ataattcaag tgcttagata aattatgttt tctttaagtg 360
tttatggtaa actcttttaa agaaaattta atatgttata gctgaatctt ttgggtaact 420
ttaaatcttt atcatagact ctgtacatat gttcaaatta gctgcttgcc tgatgtgtgt 480
atcatcgggt ggatgacaga acaaacatat ttatgatcat gaataatgtg ctttgtaa 538

<210> 312
<211> 176
<212> DNA
<213> Homo sapiens

<400> 312
ggaggagcag ctgagagata gggtcagtga atgcggttca gcctgctacc tctcctgtct 60
tcatagaacc attgccttag aattattgta tgacacgttt tttgttggtt aagctgtaag 120
gttttgttct ttgtgaacat gggatatttg aggggagggg ggaggagta gggaag 176

<210> 313
<211> 396
<212> DNA
<213> Homo sapiens

<400> 313

```

ccagcacc cc caggccctgg gggacctggg ttctcagact gccaaagaag ccttgccatc 60
tggcgctccc atggctcttg caacatctcc ccttcgtttt tgaggggggc atgccggggg 120
agccaccagc cctcactggg gttcggagga gagtcaggaa gggccaagca cgacaaagca 180
gaaacatcgg atttggggaa cgcgtgtcaa tcccttggtc cgcagggtg ggcgggagag 240
actgttctgt tcttggtgta actgtgttgc tgaaagacta cctcgttctt gtcttgatgt 300
gtcaccgggg caactgcctg ggggcgggga tgggggcagg gtggaagcgg ctccccattt 360
tataccaaag gtgctacatc tatgtgatgg gtgggg 396

```

<210> 314

<211> 311

<212> DNA

<213> Homo sapiens

<400> 314

```

cctcaacatc ctcagagagg actggaagcc agtccttacg ataaactcca taatttatgg 60
cctgcagtat ctcttcttgg agcccaaccc cgaggacca ctgaacaagg aggccgcaga 120
ggctcctgcag aacaaccggc ggctgtttga gcagaacgtg cagcgtcca tgcggggtgg 180
ctacatcggc tccacctact ttgagcgtg cctgaaatag ggttggcgca taccaccccc 240
cgccacggcc acaagccctg gcatccctg caaatattta ttgggggcca tgggtagggg 300
tttggggggc g 311

```

<210> 315

<211> 336

<212> DNA

<213> Homo sapiens

<400> 315

```

tttagaacat ggttatcatc caagactact ctaccctgca acattgaact cccaagagca 60
aatccacatt cctcttgagt tctgcagctt ctgtgtaa ataggcagctg tctgtctatgc 120
cgtagaatca catgatctga ggaccattca tggaaagctg taaatagcct agtctgggga 180
gtcttccata aagttttgca tggagcaa acacaggatt aaactagggt tggttccttc 240
agccctctaa aagcataggg cttagcctgc aggttctctt gggctttctc tgtgtgtgta 300
gttttgtaaa cactatagca tctgttaaga tccagt 336

```

<210> 316

<211> 436

<212> DNA

<213> Homo sapiens

<400> 316

```

aacatggctc gcgtgcctta agagagacgc ttcttcgaga acaggacctg actacaaaga 60
atgtttccat tggaaattgt ggtaaagact tggagtttac aatctatgat gatgatgatg 120
tgtctccatt cctggaaggt cttgaagaaa gaccacagag aaaggcacag cctgctcaac 180
ctgctgatga acctgcagaa aaggctgatg aaccaatgga acattaagtg ataagccagt 240
ctatatatgt attatcaa atgtagaat acaggcacca catactgatg acaataatct 300
atactttgaa ccaaaagt cagagtgtg gaatgctatg ttttaggaat cagtccagat 360
gtgagttttt tccaagcaac ctactgaaa cctatataat ggaatacatt tttctttgaa 420
agggtctgta taatca 436

```

<210> 317

<211> 196

<212> DNA

<213> Homo sapiens

<400> 317

```

tattccttgt gaagatgata tactatTTTT gttaagcgtg tctgtattta tgtgtgagga 60

```

```

gctgctgget tgcagtgcgc gtgcacgtgg agagctggtg cccggagatt ggacggcctg 120
atgctccctc ccctgccctg gtccaggga gctggccgag ggtcctggct cctgaggggc 180
atctgcccct ccccca                                     196

```

<210> 318

<211> 381

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 8, 9, 102, 122, 167, 182, 193, 235, 253, 265, 266, 290, 321, 378

<223> n = A,T,C or G

<400> 318

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gacgcttnng ccgtaacgat gatcggagac atcctgctgt tcgggacgtt gctgatgaat 60
gccggggcgg tgctgaactt taagctgaaa aagaaggaca cncagggcct tggggaggag 120
tncagggagc ccaacacagg tgacaacatc cggaattct tgctgancct cagatacttt 180
cnaatcttca tcncctgtg gaacatcttc atgatgttct gcatgattgt gctgntcggc 240
tcttgaatcc cancgatgaa accannaact cactttccc ggatgccgan tctccattcc 300
tccattcctg atgacttcaa naatgttttt gaccaaaaaa ccgacaacct tcccagaaa 360
tccaagctcg tggtggnngg a                                     381

```

<210> 319

<211> 506

<212> DNA

<213> Homo sapiens

<400> 319

```

ctaagcttta cgaatggggg gacaacttat gataaaaact agagctagtg aattagccta 60
tttgtaaata cctttgttat aattgatagg atacatcttg gacatggaat tgtaagcca 120
cctctgagca gtgtatgtca ggacttggtc attagggttg cagcagagg gcagaaggaa 180
ttatacaggt agagatgtat gcagatgtgt ccatatatgt ccatatttac attttgatag 240
ccattgatgt atgcatctct tggctgtact ataagaacac attaatcaa tggaaatata 300
ctttgcta attttaaatgg tatagatctg ctaatgaatt ctcttaaaaa catactgtat 360
tctgttgctg tgtgtttcat tttaaattga gcattaaggg aatgcagcat ttaaatacaga 420
actctgcaa tgcttttatc tagaggcgtg ttgccatttt tgtcttatat gaaatttctg 480
tccaagaaa ggcaggatta catctt                                     506

```

<210> 320

<211> 351

<212> DNA

<213> Homo sapiens

<400> 320

```

ctgacctgca ggacgaaacc atgaagagcc tgatccttct tgccatcctg gccgccttag 60
cggtagtaac tttgtgttat gaatcacatg aaagcatgga atcttatgaa cttaatccct 120
tcatataacag gagaaatgca aataccttca tatccctca gcagagatgg agagctaaa 180
tccaagagag gatccgagaa cgctctaagc ctgtccacga gctcaatagg gaagcctgtg 240
atgactacag actttgcgaa cgctacgcca tggtttatgg atacaatgct gcctataatc 300
gctacttcag gaagcgccga gggaccaaat gagactgagg gaagaaaaaa a 351

```

<210> 321

<211> 421

<212> DNA

<213> Homo sapiens

<400> 321

```

ctcggaggcg ttcagctgct tcaagatgaa gctgaacatc tccttcccag ccactggctg 60
ccagaaactc attgaagtgg acgatgaacg caaacttcgt actttctatg agaagcgtat 120
ggccacagaa gttgctgctg acgctctggg tgaagaatgg aagggttatg tgggccgaat 180
cagtgggtgg aacgacaaac aagggttccc catgaagcag ggtgtcttga cccatggccg 240
tgtccgctcg ctactgagta aggggcattc ctgttacaga ccaaggagaa ctggagaaag 300
aaagagaaaa tcagttcgtg gttgcattgt ggatgcaaat ctgagcgttc tcaacttggt 360
tattgtaaaa aaaggagaga aggatattcc tggactgact gatactacag tgcctcgccg 420
c 421

```

<210> 322

<211> 521

<212> DNA

<213> Homo sapiens

<400> 322

```

agcagctctc ctgccacagc tctcaccccc ctgaaaatgt tcgctgctc caagtttgtc 60
tccactccct ccttggtcaa gagcacctca cagctgctga gccgtccgct atctgcagtg 120
gtgctgaaac gaccggagat actgacagat gagagcctca gcagcttggc agtctcatgt 180
ccccttacct cacttgcttc tagccgcagc ttccaaacca gcgccatttc aaggacatc 240
gacacagcag ccaagttcat tggagctggg gctgccacag ttgggggtggc tggttctggg 300
gctgggattg gaactgtgtt tgggagcctc atcattggtt atgccaggaa cccttctctg 360
aagcaacagc tcttctccta cgccattctg ggctttgcc tctcgaggc catggggctc 420
ttttgtctga tggtagcctt tctcatcctc tttgccatgt gaaggagccg tctccacctc 480
ccatagttct cccgcgtctg gttggccccg tgtgttcctt t 521

```

<210> 323

<211> 435

<212> DNA

<213> Homo sapiens

<400> 323

```

ccgaggtcgc acgcgtgaga cttctccgcc gcagacgccg ccgcgatgcg ctacgtcgcc 60
tctacctgc tggctgccct agggggcaac tctccccca gcgccaagga catcaagaag 120
atcttgaca gcgtgggtat cgagggcgac gacgaccggc tcaacaaggt tatcagtga 180
ctgaatggaa aaaacattga agacgtcatt gccagggta ttggcaagct tgccagtga 240
cctgctgggt gggctgtagc cgtctctgct gccccaggct ctgcagcccc tgctgctggt 300
tctgccccct ctgcagcaga ggagaagaaa gatgagaaga aggaggagtc tgaagagtca 360
gatgatgaca tgggatttgg cctttttgat taaattcctg ctccccgca aataaagcct 420
ttttacacat ctcaa 435

```

<210> 324

<211> 521

<212> DNA

<213> Homo sapiens

<400> 324

```

aggagatcga ctttcggtgc ccgcaagacc agggctggaa cgccgagatc acgctgcaga 60
tgggtgcagta caagaatcgt caggccatcc tggcggtcaa atccacgcg cagaagcagc 120
agcacctggt ccagcagcag cccccctcgc agccgcagcc gcagccgcag ctccagcccc 180
aaccacagcc tcagcctcag ccgcaacccc agccccaatc acaaccccag cctcagcccc 240
aaccacagcc tcagcccccag cagctccacc cgtatccgca tccacatcca catccacact 300
ctcatcctca ctgcacccca caccctcacc cgcacccgca tccgcaccaa ataccgcacc 360
cacacccaca gccgcactcg cagccgcacg ggcaccggct tctccgcagc acctccaact 420
ctgcctgaaa ggggcagctc ccgggcaaga caagggtttg aggacttgag gaagtgggac 480
gagcacattt ctattgtctt cacttgatc aaaaagcaaaa c 521

```

<210> 325

<211> 451
 <212> DNA
 <213> Homo sapiens

<400> 325
 attttcattt ccattaacct ggaagctttc atgaatattc tcttctttta aaacatttta 60
 acattatttta aacagaaaaa gatgggctct ttctgggttag ttgttacatg atagcagaga 120
 tatttttact tagattactt tgggaatgag agattgttgt cttgaactct ggcactgtac 180
 agtgaatgtg tctgtagttg tgtagtttg cattaagcat gtataacatt caagtatgtc 240
 atccaaataa gaggcataata cattgaattg tttttaatcc tctgacaagt tgactcttcg 300
 acccccaccc ccaccaaga cattttaata gtaaataagag agagagagaa gagttaatga 360
 acatgaggta gtgttcact ggcaggatga cttttcaata gctcaaatca atttcagtgc 420
 ctttatcact tgaattatta acttaatttg a 451

<210> 326
 <211> 421
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 296
 <223> n = A,T,C or G

<400> 326
 cgcggtcgta agggctgagg atttttggtc cgcacgctcc tgctcctgac tcaccgctgt 60
 tcgctctcgc cgaggaaaca gtcggtcagg aagcccgcgc gcaacagcca tggcttttaa 120
 ggataccgga aaaacacccg tggagccgga ggtggcaatt caccgaattc gaatcaccct 180
 aacaagccgc aacgtaaaaa ccttgaaaaa ggtgtgtgct gacttgataa gaggcgcaaa 240
 agaaaagaat ctcaaagtga aaggaccagt tcgaatgcct accaagactt tgagantcac 300
 tacaagaaaa actccttgtg gtgaagggtc taagacgtgg gatcgtttcc agatgagaat 360
 tcacaagcga ctcattgact tgcacagtcc ttctgagatt gttaagcaga ttacttccat 420
 c 421

<210> 327
 <211> 456
 <212> DNA
 <213> Homo sapiens

<400> 327
 atcttgacga ggctgcggtg tctgctgcta ttctccgagc ttcgcaatgc cgcctaagga 60
 cgacaagaag aagaaggacg ctggaaagtc ggccaagaaa gacaaagacc cagtgaacaa 120
 atccgggggc aaggccaaaa agaagaagtg gtccaaaggc aaagtctcggg acaagctcaa 180
 taacttagtc ttgtttgaca aagctaccta tgataaactc tgtaagggaag ttcccaacta 240
 taaacttata accccagctg tggctctctga gagactgaag attcgaggct ccctggccag 300
 ggcagccctt caggagctcc ttagtaaagg acttatcaaa ctggtttcaa agcacagagc 360
 tcaagtaatt tacaccagaa ataccaaggg tggagatgct ccagctgctg gtgaagatgc 420
 atgaataggt ccaaccagct gtacatttgg aaaaat 456

<210> 328
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 328
 gtggaagtga catcgtcttt aaaccctgcg tggcaatccc tgacgcaccg ccgtgatgcc 60
 cagggaagac agggcgacct ggaagtccaa ctacttcctt aagatcatcc aactattgga 120
 tgattatccg aaatgtttca ttgtgggagc agacaatgtg ggctccaagc agatgcagca 180

```

gatccgcatg tcccttcgcg ggaaggctgt ggtgctgatg ggcaagaaca ccatgatgcg 240
caaggccatc cgagggcacc tggaaaacaa cccagctctg gagaaactgc tgcctcatat 300
ccgggggaat gtgggctttg tgttcaccaa ggaggacctc actgagatca gggacatgtt 360
gctggccaat aagggtgccag ctgctgcccg tctggtgcc attgccccat gtgaagtcac 420
tgtgccagcc cagaacactg gtctcgggcc cgagaagacc tcctttttcc a 471

```

<210> 329
 <211> 278
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 154, 204
 <223> n = A,T,C or G

```

<400> 329
gtttaaactt aagcttgcta ccgagctcgg atccactagt ccagtgtggt ggaattctag 60
aaattgagat gcccccccag gccagcaaat gttccttttt gttcaaagtc tatttttatt 120
ccttgatatt tttctttttt tttttttttt ttgnggatgg ggacttgtga atttttctaa 180
aggtgctatt taacatggga gganagcgtg tgcggtcca gccagcccg ctgctcactt 240
tccacctct ctccacctgc ctctggcttc tcaggcct 278

```

<210> 330
 <211> 338
 <212> DNA
 <213> Homo sapiens

```

<400> 330
ctcaggcttc aacatcgaat acgcccagc ccccttcgcc ctattcttca tagccgaata 60
cacaaacatt attataataa acaccctcac cactacaatc ttctaggaa caacatatga 120
cgcaactctc cctgaactct acacaacata ttttgtcacc aagaccctac ttctaacctc 180
cctgttctta tgaattcgaa cagcatacc ccgattccgc tacgaccaac tcatacacct 240
cctatgaaaa aacttcctac cactaccctc agcattactt atatgatatg tctccatacc 300
cattacaatc tccagcattc cccctcaaac ctaaaaaa 338

```

<210> 331
 <211> 2820
 <212> DNA
 <213> Homo sapiens

```

<400> 331
tggaacaaatc ctggagccag aagaaaggac agcagcattg atcaatctta cagctaacat 60
gttgtacctg gaaaacaatg cccagactca atttagttag ccacagtaca cgaacctggg 120
gtcctgaac agcatggacc agcagattcg gaacggctcc tcgtccacca gtccctataa 180
cacagaccac ggcgagaaca ggcgcacggc gccctcgccc tacgcacagc ccagccccac 240
cttcgatgct ctctctccat caccgcccac cccctccaac accgactacc caggcccgcg 300
cagttccgac gtgtccttcc agcagtcgag caccgccaag tcggccacct ggacgtattc 360
cactgaactg aagaaactct actgccaaat tgcaaagaca tgccccatcc agatcaagggt 420
gatgacccca cctctcagg gagctgttat ccgcgccatg cctgtctaca aaaaagctga 480
gcacgtcacg gaggtggtga agcgggtgcc caaccatgag ctgagccgtg agttcaacga 540
gggacagatt gccctccta gtcatttgat tgcagtagag gggaacagcc atgccagta 600
tgtagaagat cccatcacag gaagacagag tgtgtgtgta ccttatgagc caccccaagg 660
tggcactgaa ttcacgacag tcttgtacaa tttcatgtgt aacagcagtt gtgttgagg 720
gatgaaccgc cgtccaattt taatcattgt tactctggaa accagagatg ggcaagtcct 780
gggcccagcg tgctttgagg cccggatctg tgcttgcca ggaagagaca ggaaggcgga 840
tgaagatagc atcagaaagc agcaagtttc ggacagtaca aagaacggtg atggtacgaa 900
gcgcccgttt cgtcagaaca cacatggtat ccagatgaca tccatcaaga aacgaagatc 960

```

```

cccagatgat gaactgttat acttaccagt gagggggccgt gagacttatg aaatgctgtt 1020
gaagatcaaa gagtccctgg aactcatgca gtaccttcct cagcacacaa ttgaaacgta 1080
caggcaacag caacagcagc agcaccagca cttacttcag aaacagacct caatacagtc 1140
tccatcttca tatggtaaca gctccccacc tctgaacaaa atgaacagca tgaacaagct 1200
gccttctgtg agccagctta tcaacctca gcagcgcaac gccctcactc ctacaaccat 1260
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ccactgcaca cccccacctc cgtatcccac agattgcagc attgtcagtt tcttagcgag 1440
gttgggctgt tcatcatgtc tggactatth cagaccagc gggctgacca ccatctatca 1500
gattgagcat tactccatgg atgatctggc aagctgaaa atccctgagc aatttcgaca 1560
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tctcctgagg acccaagca gtgcctctac agtcagtggt ggctccagtg agaccggggg 1680
tgagcgtgtt attgatgctg tgcgattcac cctccgccag accatctctt tcccaccccg 1740
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caaagaggag ggggagtgg cctcaccatg tgagctcttc ctatccctct cctaactgcc 1860
agccccctaa aagcactcct gcttaatctt caaagccttc tccctagctc ctcccccttc 1920
tcttgtctga tttcttaggg gaaggagaag taaggaggta cctcttacct aacatctgac 1980
ctggcatcta attctgattc tggctttaag ccttcaaaac tatagcttgc agaactgtag 2040
ctgcatggc taggtagaag tgagcaaaaa agagttgggt gtctccttaa gctgcagaga 2100
tttctcattg acttttataa agcatgttca cccttatagt ctaagactat atatataaat 2160
gtataaatat acagtataga tttttgggtg gggggcattg agtattgttt aaaatgtaat 2220
ttaaatgaaa gaaaattgag ttgcacttat tgaccatttt ttaatttact tgttttggat 2280
ggcttgtcta tactccttcc cttaaggggt atcatgtatg gtgataggta tctagagctt 2340
aatgctacat gtgagtgcga tgatgtacag attccttcag ttctttggat tctaaatata 2400
tgccacatca aacctttgag tagatccatt tccattgctt attatgtagg taagactgta 2460
gatatgtatt cttttctcag tgttggtata ttttatatta ctgacatttc ttctagtgt 2520
gatggttcac gttgggggtga tttaatccag ttataagaag aagttcatgt ccaaacggtc 2580
ctcttttagt tttgggtggg aatgaggaaa attcttaaaa ggcccatagc agccagttca 2640
aaaacacccg acgtcatgta tttgagcata tcagtaaccc ccttaaattt aatacccaga 2700
taccttatct tacaatgttg attgggaaaa catttgctgc ccattacaga ggtattaaaa 2760
ctaaatttca ctactagatt gactaactca aatacacatt tgctactgtt gtaagaattc 2820

```

<210> 332

<211> 2270

<212> DNA

<213> Homo sapiens

<400> 332

```

tcgttgatat caaagacagt tgaaggaaat gaattttgaa acttcacggt gtgccaccct 60
acagtactgc cctgaccctt acatccagcg ttctgtagaa acccagctca tttctcttgg 120
aaagaaagtt attaccgatc caccatgtcc cagagcacac agacaaatga attcctcagt 180
ccagagggtt tccagcatat ctgggatttt ctggaacagc ctatatgttc agttcagccc 240
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<211> 2816

<212> DNA

<213> Homo sapiens

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<210> 334

<211> 2082

<212> DNA

<213> Homo sapiens

<400> 334

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<211> 1386

<212> DNA

<213> Homo sapiens

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aaactctact gccaaattgc aaagacatgc cccatccaga tcaaggtgat gacccacct 540
cctcagggag ctgttatccg cgccatgcct gtctacaaa aagctgagca cgtcacggag 600
gtggtgaagc ggtgccccaa ccatgagctg agccgtgaat tcaacgaggg acagattgcc 660
cctcctagtc atttgattcg agtagagggg aacagccatg cccagtatgt agaagatccc 720
atcacaggaa gacagagtggt gctggtacct tatgagccac cccaggttgg cactgaattc 780
acgacagtct tgtacaattt catgtgtaac agcagttgtg ttggagggat gaaccgctgt 840
ccaattttaa tcattgttac tctggaacc agagatgggc aagtcctggg ccgacgctgc 900
tttgaggccc ggatctgtgc ttgcccagga agagacagga aggcggatga agatagcatc 960
agaaagcagc aagtttcgga cagtacaaag aacggtgatg gtacgaagcg cccgtttcgt 1020
cagaacacac atggtatcca gatgacatcc atcaagaaac gaagatcccc agatgatgaa 1080
ctgttatact taccagttag gggccgtgag acttatgaaa tgctgttgaa gatcaaagag 1140
tccctggaac tcattgcagta ccttctctag cacacaattg aaacgtacag gcaacagcaa 1200
cagcagcagc accagcactt acttcagaaa cagacctcaa tacagtctcc atcttcatat 1260
ggtaacagct cccacacctt gaacaaaatg aacagcatga acaagctgcc ttctgtgagc 1320
cagcttatca accctcagca gcgcaacgcc ctactccta caaccattcc tgatggcatg 1380
ggagccaaca ttcccatgat gggcaccac atgccaatgg ctggagacat gaatggactc 1440
agccccacc aggcactccc tccccactc tccatgccat ccacctccca ctgcacaccc 1500
ccacctccgt atcccacaga ttgcagcatt gtcaggatct ggcaagtctg a 1551

<210> 338

<211> 586

<212> PRT

<213> Homo sapiens

<400> 338

Met	Leu	Tyr	Leu	Glu	Asn	Asn	Ala	Gln	Thr	Gln	Phe	Ser	Glu	Pro	Gln
1				5				10					15		
Tyr	Thr	Asn	Leu	Gly	Leu	Leu	Asn	Ser	Met	Asp	Gln	Gln	Ile	Arg	Asn
		20					25						30		
Gly	Ser	Ser	Ser	Thr	Ser	Pro	Tyr	Asn	Thr	Asp	His	Ala	Gln	Asn	Ser
		35					40					45			
Val	Thr	Ala	Pro	Ser	Pro	Tyr	Ala	Gln	Pro	Ser	Pro	Thr	Phe	Asp	Ala
		50				55					60				
Leu	Ser	Pro	Ser	Pro	Ala	Ile	Pro	Ser	Asn	Thr	Asp	Tyr	Pro	Gly	Pro
65					70					75				80	
His	Ser	Ser	Asp	Val	Ser	Phe	Gln	Gln	Ser	Ser	Thr	Ala	Lys	Ser	Ala
			85						90					95	
Thr	Trp	Thr	Tyr	Ser	Thr	Glu	Leu	Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala
			100					105					110		
Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	Val	Met	Thr	Pro	Pro	Pro	Gln	Gly
		115					120						125		

Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160
 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445
 Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys
 450 455 460
 Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr
 465 470 475 480
 Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro
 485 490 495
 Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln
 500 505 510
 Leu His Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser
 515 520 525
 Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
 530 535 540
 Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro
 545 550 555 560
 Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn
 565 570 575
 Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
 580 585

<210> 339
 <211> 641
 <212> PRT
 <213> Homo sapiens

<400> 339

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Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1           5           10          15
Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
          20          25          30
Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
          35          40          45
Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
          50          55          60
Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
          65          70          75          80
Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
          85          90          95
Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
          100         105         110
Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
          115         120         125
Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
          130         135         140
Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
          145         150         155         160
Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
          165         170         175
Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
          180         185         190
Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
          195         200         205
Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
          210         215         220
Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
          225         230         235         240
Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
          245         250         255
Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
          260         265         270
Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
          275         280         285
Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
          290         295         300
Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
          305         310         315         320
Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
          325         330         335
Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
          340         345         350
Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
          355         360         365
Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
          370         375         380
Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
          385         390         395         400

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146

Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495
 His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Gly
 500 505 510
 Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
 515 520 525
 Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
 530 535 540
 Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
 545 550 555 560
 Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His
 565 570 575
 Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser
 580 585 590
 Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
 595 600 605
 Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe
 610 615 620
 Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
 625 630 635 640
 Glu

<210> 340

<211> 448

<212> PRT

<213> Homo sapiens

<400> 340

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15
 Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30
 Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45
 Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60
 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80
 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95
 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140

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Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
145          150          155          160
Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
          165          170          175
Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
          180          185          190
Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
          195          200          205
Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
210          215          220
Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
225          230          235          240
Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
          245          250          255
Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
          260          265          270
Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
          275          280          285
Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
290          295          300
Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
305          310          315          320
Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
          325          330          335
Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
          340          345          350
Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
          355          360          365
Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
          370          375          380
Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
385          390          395          400
Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys
          405          410          415
Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser
          420          425          430
Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro
          435          440          445

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<210> 341

<211> 356

<212> PRT

<213> Homo sapiens

<400> 341

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Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
1          5          10          15
Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
          20          25          30
Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
          35          40          45
Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
          50          55          60
Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
65          70          75          80
His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
          85          90          95

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Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Gln Gly
 115 120 125
 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160
 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Ser Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln
 355

<210> 342

<211> 680

<212> PRT

<213> Homo sapiens

<400> 342

Met Asn Phe Glu Thr Ser Arg Cys Ala Thr Leu Gln Tyr Cys Pro Asp
 1 5 10 15
 Pro Tyr Ile Gln Arg Phe Val Glu Thr Pro Ala His Phe Ser Trp Lys
 20 25 30
 Glu Ser Tyr Tyr Arg Ser Thr Met Ser Gln Ser Thr Gln Thr Asn Glu
 35 40 45
 Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
 50 55 60
 Pro Ile Cys Ser Val Gln Pro Ile Asp Leu Asn Phe Val Asp Glu Pro
 65 70 75 80
 Ser Glu Asp Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile
 85 90 95
 Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr
 100 105 110
 Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser
 115 120 125

Ser	Ser	Thr	Ser	Pro	Tyr	Asn	Thr	Asp	His	Ala	Gln	Asn	Ser	Val	Thr	130	135	140
Ala	Pro	Ser	Pro	Tyr	Ala	Gln	Pro	Ser	Ser	Thr	Phe	Asp	Ala	Leu	Ser	145	150	155
Pro	Ser	Pro	Ala	Ile	Pro	Ser	Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	Ser	165	170	175
Phe	Asp	Val	Ser	Phe	Gln	Gln	Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	180	185	190
Thr	Tyr	Ser	Thr	Glu	Leu	Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	195	200	205
Cys	Pro	Ile	Gln	Ile	Lys	Val	Met	Thr	Pro	Pro	Pro	Gln	Gly	Ala	Val	210	215	220
Ile	Arg	Ala	Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	Glu	Val	225	230	235
Val	Lys	Arg	Cys	Pro	Asn	His	Glu	Leu	Ser	Arg	Glu	Phe	Asn	Glu	Gly	245	250	255
Gln	Ile	Ala	Pro	Pro	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Ser	His	260	265	270
Ala	Gln	Tyr	Val	Glu	Asp	Pro	Ile	Thr	Gly	Arg	Gln	Ser	Val	Leu	Val	275	280	285
Pro	Tyr	Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Val	Leu	Tyr	290	295	300
Asn	Phe	Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	305	310	315
Ile	Leu	Ile	Ile	Val	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly	325	330	335
Arg	Arg	Cys	Phe	Glu	Ala	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	340	345	350
Lys	Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp	Ser	Thr	355	360	365
Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr	His	Gly	370	375	380
Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp	Glu	Leu	385	390	395
Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu	Leu	Lys	405	410	415
Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro	Gln	His	Thr	Ile	420	425	430
Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Leu	Leu	Gln	435	440	445
Lys	Gln	Thr	Ser	Ile	Gln	Ser	Pro	Ser	Ser	Tyr	Gly	Asn	Ser	Ser	Pro	450	455	460
Pro	Leu	Asn	Lys	Met	Asn	Ser	Met	Asn	Lys	Leu	Pro	Ser	Val	Ser	Gln	465	470	475
Leu	Ile	Asn	Pro	Gln	Gln	Arg	Asn	Ala	Leu	Thr	Pro	Thr	Thr	Ile	Pro	485	490	495
Asp	Gly	Met	Gly	Ala	Asn	Ile	Pro	Met	Met	Gly	Thr	His	Met	Pro	Met	500	505	510
Ala	Gly	Asp	Met	Asn	Gly	Leu	Ser	Pro	Thr	Gln	Ala	Leu	Pro	Pro	Pro	515	520	525
Leu	Ser	Met	Pro	Ser	Thr	Ser	Gln	Cys	Thr	Pro	Pro	Pro	Pro	Tyr	Pro	530	535	540
Thr	Asp	Cys	Ser	Ile	Val	Ser	Phe	Leu	Ala	Arg	Leu	Gly	Cys	Ser	Ser	545	550	555
Cys	Leu	Asp	Tyr	Phe	Thr	Thr	Gln	Gly	Leu	Thr	Thr	Ile	Tyr	Gln	Ile	565	570	575
Glu	His	Tyr	Ser	Met	Asp	Asp	Leu	Ala	Ser	Leu	Lys	Ile	Pro	Glu	Gln	580	585	590

150

Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His
 595 600 605
 Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser Ala Ser
 610 615 620
 Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp
 625 630 635 640
 Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp
 645 650 655
 Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn Lys Gln
 660 665 670
 Gln Arg Ile Lys Glu Glu Gly Glu
 675 680

<210> 343

<211> 461

<212> PRT

<213> Homo sapiens

<400> 343

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Gln Gly
 115 120 125
 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160
 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300

151

Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445
 Tyr Pro Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val
 450 455 460

<210> 344

<211> 516

<212> PRT

<213> Homo sapiens

<400> 344

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15
 Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30
 Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45
 Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60
 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80
 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95
 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140
 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240

Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495
 His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Arg
 500 505 510
 Ile Trp Gln Val
 515

<210> 345

<211> 1800

<212> DNA

<213> Homo sapiens

<400> 345

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 tgacattcgt atcatcactg tgcaccattg gcttctaggc actccagtgg ggtaggagaa 180
 ggaggtctga aaccctcgca gagggatctt gccctcattc tttgggtctg aaacactggc 240
 agtcgttgga aacaggactc agggataaac cagcgcaatg gattggggga cgctgcacac 300
 tttcatcggg ggtgtcaaca aacactccac cagcatcggg aaggtgtgga tcacagtcac 360
 ctttattttc cgagtcata tctagtgtgt ggctgcccag gaagtgtggg gtgacgagca 420
 agaggacttc gtctgcaaca cactgcaacc gggatgcaaa aatgtgtgct atgaccactt 480
 tttcccggtg tcccacatcc ggctgtgggc cctccagctg atcttctgtt ccaccccagc 540
 gctgtgtgtg gccatgcatg tggcctacta caggcacgaa accactcgca agttcaggcg 600
 aggagagaag aggaatgatt tcaaagacat agaggacatt aaaaagcaca aggttcggat 660
 agaggggtcg ctgtgttgga cgtacaccag cagcatcttt ttccgaatca tctttgaagc 720
 agcctttatg tatgtgtttt acttccttta caatgggtac cacctgcctt ggggtgtgaa 780
 atgtgggatt gaccctgcc ccaaccttgt tgactgcttt atttctaggc caacagagaa 840

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gaccgtgttt accattttta tgattttctgc gtctgtgatt tgcattgctgc ttaacgtggc 900
agagttgtgc tacctgctgc tgaaagtgtg ttttaggaga tcaaagagag cacagacgca 960
aaaaaatcac cccaatcatg ccctaaagga gagtaagcag aatgaaatga atgagctgat 1020
ttcagatagt ggtcaaaatg caatcacagg tttccaagc taaacatttc aaggtaaaat 1080
gtagctgcgt cataaggaga cttctgtctt ctccagaagg caataccaac ctgaaagtcc 1140
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gactctctga caaagtgggt actttctgaa aatttatata actgtgtgtg ataaggaaca 1380
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tacgcttaag gtgggaaagt gttcattgca caatatatatt ttactgcttt ctgaatgtag 1680
acggaacagt gtggaagcag aaggcttttt taactcatcc gtttggccga tcgttgacga 1740
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<210> 346

<211> 261

<212> PRT

<213> Homo sapiens

<400> 346

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Met Asp Trp Gly Thr Leu His Thr Phe Ile Gly Gly Val Asn Lys His
 1          5          10          15
Ser Thr Ser Ile Gly Lys Val Trp Ile Thr Val Ile Phe Ile Phe Arg
          20          25          30
Val Met Ile Leu Val Val Ala Ala Gln Glu Val Trp Gly Asp Glu Gln
          35          40          45
Glu Asp Phe Val Cys Asn Thr Leu Gln Pro Gly Cys Lys Asn Val Cys
          50          55          60
Tyr Asp His Phe Phe Pro Val Ser His Ile Arg Leu Trp Ala Leu Gln
          65          70          75          80
Leu Ile Phe Val Ser Thr Pro Ala Leu Leu Val Ala Met His Val Ala
          85          90          95
Tyr Tyr Arg His Glu Thr Thr Arg Lys Phe Arg Arg Gly Glu Lys Arg
          100          105          110
Asn Asp Phe Lys Asp Ile Glu Asp Ile Lys Lys His Lys Val Arg Ile
          115          120          125
Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser Ile Phe Phe Arg Ile
          130          135          140
Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr Phe Leu Tyr Asn Gly
          145          150          155          160
Tyr His Leu Pro Trp Val Leu Lys Cys Gly Ile Asp Pro Cys Pro Asn
          165          170          175
Leu Val Asp Cys Phe Ile Ser Arg Pro Thr Glu Lys Thr Val Phe Thr
          180          185          190
Ile Phe Met Ile Ser Ala Ser Val Ile Cys Met Leu Leu Asn Val Ala
          195          200          205
Glu Leu Cys Tyr Leu Leu Leu Lys Val Cys Phe Arg Arg Ser Lys Arg
          210          215          220
Ala Gln Thr Gln Lys Asn His Pro Asn His Ala Leu Lys Glu Ser Lys
          225          230          235          240
Gln Asn Glu Met Asn Glu Leu Ile Ser Asp Ser Gly Gln Asn Ala Ile
          245          250          255
Thr Gly Phe Pro Ser
          260

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<210> 347
 <211> 1740
 <212> DNA
 <213> Homo sapiens

<400> 347
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 atcttcaagg acgccaagat cccggtgtcg ggaccttcc tggatgaagac tggctacgcg 120
 ttcgtggact gcccgacga gagctgggccc ctcaaggcca tcgaggcgct ttcaggtaaa 180
 atagaactgc acgggaaacc catagaagt gagcactcgg tccccaaaag gcaaaggatt 240
 cggaacttc agatacgaat tatccgcct catttacagt gggaggtgct ggatagtta 300
 ctagtccagt atggagtggg ggagagctgt gagcaagtga aactgactc ggaaactgca 360
 gttgtaaatg taacctattc cagtaaggac caagctagac aagcactaga caaactgaat 420
 ggatttcagt tagagaattt caccctgaaa gtacgtata tccctgatga aacggccgcc 480
 cagcaaaacc ccttgacga gcccgagggt cggcgggggt ttgggcagag gggctcctca 540
 aggcaggggt ctccaggatc cgtatccaag cagaaccat gtgatttgcc tctgcgctcg 600
 ctggttccca ccaatttgt tggagccatc ataggaaaag aaggtgccac cattcggaac 660
 atcaccaaac agaccagtc taaaatcgat gtccaccgta aagaaaatgc gggggctgct 720
 gagaagtcca ttactatcct ctctactcct gaaggcacct ctgcgcttg taagtctatt 780
 ctggagatta tgcataagga agctcaagat ataaaattca cagaagatg ccccttgaag 840
 attttagctc ataataactt tgttgacgt cttattggta aagaaggaag aaatcttaaa 900
 aaaattgagc aagacacaga cactaaaatc acgatatcct cattgcagga attgacgctg 960
 tataatccag aacgcactat tacagttaaa ggcaatgttg agacatgtgc caaagctgag 1020
 gaggagatca tgaagaaat caggagatct tatgaaaatg atattgcttc tatgaatctt 1080
 caagcacatt taattcctgg attaaatctg aacgccttgg gtctgttccc acccacttca 1140
 gggatgccac ctcccacctc agggccctc tccagcatga ctctccctca cccgcagttt 1200
 gagcaatcag aaacggagac tgttcactcg tttatccag ctctatcagt cggtgccatc 1260
 atcggaagc agggccaagc catcaagcag ctttctcgt ttgctggagc ttcaattaag 1320
 attgctccag cggaagcacc agatgctaaa gtgaggatgg tgattatcac tggaccacca 1380
 gaggtcagt tcaaggctca gggaagaatt tatggaaaaa ttaagaaga aaactttgtt 1440
 agtcctaaag aagaggtgaa acttgaagct catatcagag tgccatcctt tgctgctggc 1500
 agagttattg gaaaaggagg caaaacggtg aatgaacttc agaatttgct aagtgcagaa 1560
 gttgtgtcc ctctgacca gacacctgat gagaatgacc aagtggttgt caaaataact 1620
 ggtcattct atgcttgcca ggttgccag agaaaaattc aggaattct gactcaggta 1680
 aagcagcacc aacaacagaa ggctctgcaa agtgaccac ctcagtcaag acggaagtaa 1740

<210> 348
 <211> 579
 <212> PRT
 <213> Homo sapiens

<400> 348
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 Asp Leu Glu Ser Ile Phe Lys Asp Ala Lys Ile Pro Val Ser Gly Pro
 20 25 30
 Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
 35 40 45
 Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
 50 55 60
 Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile
 65 70 75 80
 Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
 85 90 95
 Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln

			100									105									110												
Val	Asn	Thr	Asp	Ser	Glu	Thr	Ala	Val	Val	Asn	Val	Thr	Tyr	Ser	Ser																		
Lys	Asp	Gln	Ala	Arg	Gln	Ala	Leu	Asp	Lys	Leu	Asn	Gly	Phe	Gln	Leu																		
Glu	Asn	Phe	Thr	Leu	Lys	Val	Ala	Tyr	Ile	Pro	Asp	Glu	Thr	Ala	Ala																		
145					150					155					160																		
Gln	Gln	Asn	Pro	Leu	Gln	Gln	Pro	Arg	Gly	Arg	Arg	Gly	Leu	Gly	Gln	Lys																	
				165					170						175																		
Arg	Gly	Ser	Ser	Arg	Gln	Gly	Ser	Pro	Gly	Ser	Val	Ser	Lys	Gln	Lys																		
			180					185							190																		
Pro	Cys	Asp	Leu	Pro	Leu	Arg	Leu	Leu	Val	Pro	Thr	Gln	Phe	Val	Gly																		
		195					200								205																		
Ala	Ile	Ile	Gly	Lys	Glu	Gly	Ala	Thr	Ile	Arg	Asn	Ile	Thr	Lys	Gln																		
		210				215					220																						
Thr	Gln	Ser	Lys	Ile	Asp	Val	His	Arg	Lys	Glu	Asn	Ala	Gly	Ala	Ala																		
225				230					235						240																		
Glu	Lys	Ser	Ile	Thr	Ile	Leu	Ser	Thr	Pro	Glu	Gly	Thr	Ser	Ala	Ala																		
				245				250							255																		
Cys	Lys	Ser	Ile	Leu	Glu	Ile	Met	His	Lys	Glu	Ala	Gln	Asp	Ile	Lys																		
			260				265								270																		
Phe	Thr	Glu	Glu	Ile	Pro	Leu	Lys	Ile	Leu	Ala	His	Asn	Asn	Phe	Val																		
		275				280									285																		
Gly	Arg	Leu	Ile	Gly	Lys	Glu	Gly	Arg	Asn	Leu	Lys	Lys	Ile	Glu	Gln																		
		290				295					300																						
Asp	Thr	Asp	Thr	Lys	Ile	Thr	Ile	Ser	Pro	Leu	Gln	Glu	Leu	Thr	Leu																		
305				310					315						320																		
Tyr	Asn	Pro	Glu	Arg	Thr	Ile																											

156

565 570 575
 Arg Arg Lys

 <210> 349
 <211> 207
 <212> DNA
 <213> Homo sapiens

 <400> 349
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 gctgcagcag cctccacca gcctgaggat gacatcaata cacagaggaa gaagagtcag 120
 gaaaagatga gagaagttac agactctcct gggcgacccc gagagcttac cattcctcag 180
 acttcttcac atggtgctaa cagattt 207

 <210> 350
 <211> 69
 <212> PRT
 <213> Homo sapiens

 <400> 350
 Met Trp Gln Pro Leu Phe Phe Lys Trp Leu Leu Ser Cys Cys Pro Gly
 1 5 10 15
 Ser Ser Gln Ile Ala Ala Ala Ala Ser Thr Gln Pro Glu Asp Asp Ile
 20 25 30
 Asn Thr Gln Arg Lys Lys Ser Gln Glu Lys Met Arg Glu Val Thr Asp
 35 40 45
 Ser Pro Gly Arg Pro Arg Glu Leu Thr Ile Pro Gln Thr Ser Ser His
 50 55 60
 Gly Ala Asn Arg Phe
 65

 <210> 351
 <211> 1012
 <212> DNA
 <213> Homo sapiens

 <400> 351
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 catcacacgg ccgcgtccga taacttccag ctgtcccagg gtgggcaggg attcgccatt 120
 ccgatcgggc aggcgatggc gatcgcgggc cagatcaagc ttcccaccgt tcatatcggg 180
 cctaccgcct tctcggctt ggggtgtgtc gacaacaacg gcaacggcgc acgagtccaa 240
 cgctgggtcg ggagcgctcc ggcggcaagt ctccgcatct ccaccggcga cgtgatcacc 300
 gcggtcgacg gcgctccgat caactcggcc accgcgatgg cggacgcgct taacgggcat 360
 catcccggtg acgtcatctc ggtgacctgg caaaccaagt cgggcggcac gcgtacaggg 420
 aacgtgacat tggccgaggg acccccggcc gaattcatgg attgggggac gctgcacact 480
 ttcacggggg gtgtcaacaa aactccacc agcatcggga aggtgtggat cacagtcac 540
 tttattttcc gagtcatgat cctcgtgggt gctgcccagg aagtgtgggg tgacgagcaa 600
 gaggacttcg tctgcaacac actgcaaccg ggatgcaaaa atgtgtgcta tgaccacttt 660
 ttcccgtgtg cccacatccg cctgtggggc ctccagctga tcttcgtctc caccacagcg 720
 ctgctggtgg ccatgcatgt ggcctactac aggcacgaaa ccactcgcaa gttcaggcga 780
 ggagagaaga ggaatgattt caaagacata gaggacatta aaaagcagaa gggtcggata 840
 gaggggtgac tcgagcacca ccaccaccac cactgagatc cggctgctaa caaagcccga 900
 aaggaaagctg agttggctgc tgccaccgct gagcaataac tagcataacc ccttgggggc 960
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<210> 352
 <211> 267
 <212> PRT
 <213> Homo sapiens

<400> 352
 Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
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 20 25 30
 Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
 35 40 45
 Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
 50 55 60
 Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
 65 70 75 80
 Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
 85 90 95
 Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
 100 105 110
 Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
 115 120 125
 Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Asp Trp Gly Thr Leu His
 130 135 140
 Thr Phe Ile Gly Gly Val Asn Lys His Ser Thr Ser Ile Gly Lys Val
 145 150 155 160
 Trp Ile Thr Val Ile Phe Ile Phe Arg Val Met Ile Leu Val Val Ala
 165 170 175
 Ala Gln Glu Val Trp Gly Asp Glu Gln Glu Asp Phe Val Cys Asn Thr
 180 185 190
 Leu Gln Pro Gly Cys Lys Asn Val Cys Tyr Asp His Phe Phe Pro Val
 195 200 205
 Ser His Ile Arg Leu Trp Ala Leu Gln Leu Ile Phe Val Ser Thr Pro
 210 215 220
 Ala Leu Leu Val Ala Met His Val Ala Tyr Tyr Arg His Glu Thr Thr
 225 230 235 240
 Arg Lys Phe Arg Arg Gly Glu Lys Arg Asn Asp Phe Lys Asp Ile Glu
 245 250 255
 Asp Ile Lys Lys Gln Lys Val Arg Ile Glu Gly
 260 265

<210> 353
 <211> 900
 <212> DNA
 <213> Homo sapiens

<400> 353
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 cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
 accgttcata tcgggcctac cgcttccctc ggcttgggtg ttgtcgacaa caacggcaac 180
 ggcgacagag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
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 gcgcttaacg ggcacatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
 ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ccacgaaacc 420
 actcgcaagt tcaggcgagg agagaagagg aatgatttca aagacataga ggacattaaa 480
 aagcagaagg ttccgataga ggggtcgctg tgggtggacgt acaccagcag catctttttc 540
 cgaatcatct ttgaagcagc ctttatgtat gtgttttact tcctttacaa tgggtaccac 600

158

ctgccctggg tgttgaaatg tgggattgac ccctgcccc aacctgttga ctgctttatt 660
 tctaggccaa cagagaagac cgtgtttacc atttttatga tttctgcgtc tgtgatttgc 720
 atgctgctta acgtggcaga gttgtgctac ctgctgctga aagtgtgttt taggagatca 780
 aagagagcac agacgcaaaa aaatcacccc aatcatgccc taaaggagag taagcagaat 840
 gaaatgaatg agctgatttc agatagtggc caaaatgcaa tcacagggtt cccaagctaa 900

<210> 354

<211> 299

<212> PRT

<213> Homo sapiens

<400> 354

Met	His	His	His	His	His	His	Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu
1				5					10					15	
Ser	Gln	Gly	Gly	Gln	Gly	Phe	Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala
			20					25					30		
Ile	Ala	Gly	Gln	Ile	Lys	Leu	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala
		35					40					45			
Phe	Leu	Gly	Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val
		50				55					60				
Gln	Arg	Val	Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr
65					70					75					80
Gly	Asp	Val	Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr
				85					90					95	
Ala	Met	Ala	Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser
			100					105					110		
Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr
		115					120					125			
Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	His	Glu	Thr	Thr	Arg	Lys	Phe
		130				135					140				
Arg	Arg	Gly	Glu	Lys	Arg	Asn	Asp	Phe	Lys	Asp	Ile	Glu	Asp	Ile	Lys
145					150					155					160
Lys	Gln	Lys	Val	Arg	Ile	Glu	Gly	Ser	Leu	Trp	Trp	Thr	Tyr	Thr	Ser
				165					170					175	
Ser	Ile	Phe	Phe	Arg	Ile	Ile	Phe	Glu	Ala	Ala	Phe	Met	Tyr	Val	Phe
			180				185						190		
Tyr	Phe	Leu	Tyr	Asn	Gly	Tyr	His	Leu	Pro	Trp	Val	Leu	Lys	Cys	Gly
		195				200						205			
Ile	Asp	Pro	Cys	Pro	Asn	Leu	Val	Asp	Cys	Phe	Ile	Ser	Arg	Pro	Thr
		210				215					220				
Glu	Lys	Thr	Val	Phe	Thr	Ile	Phe	Met	Ile	Ser	Ala	Ser	Val	Ile	Cys
225					230					235					240
Met	Leu	Leu	Asn	Val	Ala	Glu	Leu	Cys	Tyr	Leu	Leu	Leu	Lys	Val	Cys
				245					250					255	
Phe	Arg	Arg	Ser	Lys	Arg	Ala	Gln	Thr	Gln	Lys	Asn	His	Pro	Asn	His
			260				265						270		
Ala	Leu	Lys	Glu	Ser	Lys	Gln	Asn	Glu	Met	Asn	Glu	Leu	Ile	Ser	Asp
		275					280					285			
Ser	Gly	Gln	Asn	Ala	Ile	Thr	Gly	Phe	Pro	Ser					
		290				295									

<210> 355

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 355

ggagtacagc ttcaagacaa tggg

24

<210> 356

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 356

ccatgggaat tcattataat aattttgttc c

31

<210> 357

<211> 920

<212> PRT

<213> Homo sapiens

<400> 357

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Met Gln His His His His His His Gly Val Gln Leu Gln Asp Asn Gly
 1           5           10           15
Tyr Asn Gly Leu Leu Ile Ala Ile Asn Pro Gln Val Pro Glu Asn Gln
      20           25           30
Asn Leu Ile Ser Asn Ile Lys Glu Met Ile Thr Glu Ala Ser Phe Tyr
      35           40           45
Leu Phe Asn Ala Thr Lys Arg Arg Val Phe Phe Arg Asn Ile Lys Ile
      50           55           60
Leu Ile Pro Ala Thr Trp Lys Ala Asn Asn Asn Ser Lys Ile Lys Gln
      65           70           75           80
Glu Ser Tyr Glu Lys Ala Asn Val Ile Val Thr Asp Trp Tyr Gly Ala
      85           90           95
His Gly Asp Asp Pro Tyr Thr Leu Gln Tyr Arg Gly Cys Gly Lys Glu
      100          105          110
Gly Lys Tyr Ile His Phe Thr Pro Asn Phe Leu Leu Asn Asp Asn Leu
      115          120          125
Thr Ala Gly Tyr Gly Ser Arg Gly Arg Val Phe Val His Glu Trp Ala
      130          135          140
His Leu Arg Trp Gly Val Phe Asp Glu Tyr Asn Asn Asp Lys Pro Phe
      145          150          155          160
Tyr Ile Asn Gly Gln Asn Gln Ile Lys Val Thr Arg Cys Ser Ser Asp
      165          170          175
Ile Thr Gly Ile Phe Val Cys Glu Lys Gly Pro Cys Pro Gln Glu Asn
      180          185          190
Cys Ile Ile Ser Lys Leu Phe Lys Glu Gly Cys Thr Phe Ile Tyr Asn
      195          200          205
Ser Thr Gln Asn Ala Thr Ala Ser Ile Met Phe Met Gln Ser Leu Ser
      210          215          220
Ser Val Val Glu Phe Cys Asn Ala Ser Thr His Asn Gln Glu Ala Pro
      225          230          235          240
Asn Leu Gln Asn Gln Met Cys Ser Leu Arg Ser Ala Trp Asp Val Ile
      245          250          255
Thr Asp Ser Ala Asp Phe His His Ser Phe Pro Met Asn Gly Thr Glu
      260          265          270
Leu Pro Pro Pro Pro Thr Phe Ser Leu Val Glu Ala Gly Asp Lys Val

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160

275	280	285
Val Cys Leu Val Leu Asp Val Ser Ser Lys Met Ala Glu Ala Asp Arg		
290	295	300
Leu Leu Gln Leu Gln Gln Ala Ala Glu Phe Tyr Leu Met Gln Ile Val		
305	310	315
Glu Ile His Thr Phe Val Gly Ile Ala Ser Phe Asp Ser Lys Gly Glu		
325	330	335
Ile Arg Ala Gln Leu His Gln Ile Asn Ser Asn Asp Asp Arg Lys Leu		
340	345	350
Leu Val Ser Tyr Leu Pro Thr Thr Val Ser Ala Lys Thr Asp Ile Ser		
355	360	365
Ile Cys Ser Gly Leu Lys Lys Gly Phe Glu Val Val Glu Lys Leu Asn		
370	375	380
Gly Lys Ala Tyr Gly Ser Val Met Ile Leu Val Thr Ser Gly Asp Asp		
385	390	395
Lys Leu Leu Gly Asn Cys Leu Pro Thr Val Leu Ser Ser Gly Ser Thr		
405	410	415
Ile His Ser Ile Ala Leu Gly Ser Ser Ala Ala Pro Asn Leu Glu Glu		
420	425	430
Leu Ser Arg Leu Thr Gly Gly Leu Lys Phe Phe Val Pro Asp Ile Ser		
435	440	445
Asn Ser Asn Ser Met Ile Asp Ala Phe Ser Arg Ile Ser Ser Gly Thr		
450	455	460
Gly Asp Ile Phe Gln Gln His Ile Gln Leu Glu Ser Thr Gly Glu Asn		
465	470	475
Val Lys Pro His His Gln Leu Lys Asn Thr Val Thr Val Asp Asn Thr		
485	490	495
Val Gly Asn Asp Thr Met Phe Leu Val Thr Trp Gln Ala Ser Gly Pro		
500	505	510
Pro Glu Ile Ile Leu Phe Asp Pro Asp Gly Arg Lys Tyr Tyr Thr Asn		
515	520	525
Asn Phe Ile Thr Asn Leu Thr Phe Arg Thr Ala Ser Leu Trp Ile Pro		
530	535	540
Gly Thr Ala Lys Pro Gly His Trp Thr Tyr Thr Leu Asn Asn Thr His		
545	550	555
His Ser Leu Gln Ala Leu Lys Val Thr Val Thr Ser Arg Ala Ser Asn		
565	570	575
Ser Ala Val Pro Pro Ala Thr Val Glu Ala Phe Val Glu Arg Asp Ser		
580	585	590
Leu His Phe Pro His Pro Val Met Ile Tyr Ala Asn Val Lys Gln Gly		
595	600	605
Phe Tyr Pro Ile Leu Asn Ala Thr Val Thr Ala Thr Val Glu Pro Glu		
610	615	620
Thr Gly Asp Pro Val Thr Leu Arg Leu Leu Asp Asp Gly Ala Gly Ala		
625	630	635
Asp Val Ile Lys Asn Asp Gly Ile Tyr Ser Arg Tyr Phe Phe Ser Phe		
645	650	655
Ala Ala Asn Gly Arg Tyr Ser Leu Lys Val His Val Asn His Ser Pro		
660	665	670
Ser Ile Ser Thr Pro Ala His Ser Ile Pro Gly Ser His Ala Met Tyr		
675	680	685
Val Pro Gly Tyr Thr Ala Asn Gly Asn Ile Gln Met Asn Ala Pro Arg		
690	695	700
Lys Ser Val Gly Arg Asn Glu Glu Glu Arg Lys Trp Gly Phe Ser Arg		
705	710	715
Val Ser Ser Gly Gly Ser Phe Ser Val Leu Gly Val Pro Ala Gly Pro		
725	730	735
His Pro Asp Val Phe Pro Pro Cys Lys Ile Ile Asp Leu Glu Ala Val		

	740		745		750
Lys Val Glu Glu Leu Thr	Leu Ser Trp Thr	Ala Pro Gly Glu Asp			
755	760	765			
Phe Asp Gln Gly Gln Ala Thr	Ser Tyr Glu Ile	Arg Met Ser Lys Ser			
770	775	780			
Leu Gln Asn Ile Gln Asp Asp	Phe Asn Asn Ala Ile	Leu Val Asn Thr			
785	790	795			800
Ser Lys Arg Asn Pro Gln Gln	Ala Gly Ile Arg Glu Ile	Phe Thr Phe			
	805	810			815
Ser Pro Gln Ile Ser Thr Asn	Gly Pro Glu His Gln Pro	Asn Gly Glu			
	820	825			830
Thr His Glu Ser His Arg Ile	Tyr Val Ala Ile Arg Ala	Met Asp Arg			
	835	840			845
Asn Ser Leu Gln Ser Ala Val	Ser Asn Ile Ala Gln Ala	Pro Leu Phe			
	850	855			860
Ile Pro Pro Asn Ser Asp Pro	Val Pro Ala Arg Asp Tyr	Leu Ile Leu			
865	870	875			880
Lys Gly Val Leu Thr Ala Met	Gly Leu Ile Gly Ile Ile	Cys Leu Ile			
	885	890			895
Ile Val Val Thr His His Thr	Leu Ser Arg Lys Lys Arg	Ala Asp Lys			
	900	905			910
Lys Glu Asn Gly Thr Lys Leu	Leu				
	915	920			

<210> 358

<211> 2773

<212> DNA

<213> Homo sapiens

<400> 358

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gaaatgataa	ctgaagcttc	attttaccta	tttaatgcta	ccaagagaag	agtatttttc	180
agaaatataa	agattttta	acctgccaca	tggaaagcta	ataataacag	caaaataaaa	240
caagaatcat	atgaaaaggc	aaatgtcata	gtgactgact	ggtatggggc	acatggagat	300
gatccataca	ccctacaata	cagagggtgt	ggaaaagagg	gaaaatacat	tcatttcaca	360
cctaattttc	tactgaatga	taactttaaca	gctggctacg	gatcacgagg	ccgagtgttt	420
gtccatgaat	gggcccacct	ccgttggggg	gtgttcgatg	agtataacaa	tgacaaacct	480
ttctacataa	atggggcaaaa	tcaaattaaa	gtgacaaggt	gttcatctga	catcacaggc	540
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aaagaaggat	gcacctttat	ctacaatagc	acccaaaatg	caactgcatc	aataatgttc	660
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gttgaaattc	ataccttcgt	gggcattgcc	agtttcgaca	gcaaaggaga	gatcagagcc	1020
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gttgaaaaac	tgaatggaaa	agcttatggc	tctgtgatga	tattagtgc	cagcggagat	1200
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gacactatgt	ttctagttac	gtggcaggcc	agtggtcctc	ctgagattat	attatttgat	1560
cctgatggac	gaaaatacta	cacaaataat	tttatcacca	atctaacttt	tcggacagct	1620

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agtcttttga ttccaggaac agctaagcct gggcactgga cttacaccct gaacaatacc 1680
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atgatttatg ccaatgtgaa acagggattt tatcccattc ttaatgccac tgtcactgcc 1860
acagttgagc cagagactgg agatcctgtt acgctgagac tccttgatga tggagcaggt 1920
gctgatgtta taaaaaatga tggaaattac tcgagggtatt ttttctcctt tgctgcaaat 1980
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caggcgctc tgtttattcc cccaattct gatcctgtac ctgccagaga ttatcttata 2640
ttgaaaggag ttttaacagc aatgggtttg ataggaatca tttgccttat tatagttgtg 2700
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<210> 359

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 359

tggcagcccc tcttcttcaa gtggc

25

<210> 360

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 360

cgccagaatt catcaaaca atctgttagc acc

33

<210> 361

<211> 77

<212> PRT

<213> Homo sapiens

<400> 361

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Met Gln His His His His His Trp Gln Pro Leu Phe Phe Lys Trp
 1              5              10              15
Leu Leu Ser Cys Cys Pro Gly Ser Ser Gln Ile Ala Ala Ala Ala Ser
          20              25              30
Thr Gln Pro Glu Asp Asp Ile Asn Thr Gln Arg Lys Lys Ser Gln Glu
          35              40              45
Lys Met Arg Glu Val Thr Asp Ser Pro Gly Arg Pro Arg Glu Leu Thr
          50              55              60
Ile Pro Gln Thr Ser Ser His Gly Ala Asn Arg Phe Val

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163

65

70

75

<210> 362

<211> 244

<212> DNA

<213> Homo sapiens

<400> 362

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tggtgccctg ggagttctca aattgctgca gcagcctcca cccagcctga ggatgacatc 120
aatacacaga ggaagaagag tcaggaaaag atgagagaag ttacagactc tcctgggcga 180
ccccgagagc ttaccattcc tcagacttct tcacatgggtg ctaacagatt tgtttgatga 240
attc                                     244
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<210> 363

<211> 20

<212> PRT

<213> Homo sapiens

<400> 363

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Met Trp Gln Pro Leu Phe Phe Lys Trp Leu Leu Ser Cys Cys Pro Gly
 1             5             10            15
Ser Ser Gln Ile
                20
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<210> 364

<211> 60

<212> DNA

<213> Homo sapiens

<400> 364

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atgtggcagc ccctcttctt caagtggctc ttgtcctgtt gccctgggag ttctcaaatt 60
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<210> 365

<211> 20

<212> PRT

<213> Homo sapiens

<400> 365

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Gly Ser Ser Gln Ile Ala Ala Ala Ala Ser Thr Gln Pro Glu Asp Asp
 1             5             10            15
Ile Asn Thr Gln
                20
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<210> 366

<211> 60

<212> DNA

<213> Homo sapiens

<400> 366

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gggagttctc aaattgctgc agcagcctcc acccagcctg aggatgacat caatacacag 60
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<210> 367

164

<211> 20
 <212> PRT
 <213> Homo sapiens

<400> 367
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 1 5 10 15
 Gln Ala Leu Lys
 20

<210> 368
 <211> 2343
 <212> DNA
 <213> Homo sapiens

<400> 368
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 gcgcccgcgc tctgagcgc agcatgtgaa gcggagacgg catccagtgg ggggcgagcc 180
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 gaatatattg aacgtcttgt atggagaacc ccaggaggag gctctagagg tggacctgaa 300
 gcttttgatc ctaaaagatt attagaagaa tttgtaaatc atattcagga actccagata 360
 atggatgaaa ggattcagag gaaagtagag aaactagagc aacaatgtca gaaagaagcc 420
 aaggaatttg ccaagaaggc acaagagctg cagaaaagca atcaggttgc cttccaacat 480
 ttccaagaac tagatgagca cattagctat gtagcaacta aagtctgtca ccttggagac 540
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 tactttaatg agtttctaga tggagaattg aaatctgatg tttttacaaa ttctgaaaag 660
 ataaaggaag cagcagacat cattcagaag ttgcaccta ttgcccaaga gttacctttt 720
 gatagatttt cagaagttaa atccaaaatt gcaagtaaat accatgattt agaatgccag 780
 ctgattcagg agtttaccag tgctcaaaga agaggtgaaa tctccagaat gagagaagta 840
 gcagcagttt tacttcattt taagggttat tcccattgtg ttgatgttta tataaagcag 900
 tgccaggagg gtgcttattt gagaaatgat atatttgaag acgctggaat actctgtcaa 960
 agagtgaaca aacaagttgg agatatcttc agtaatccag aaacagtcct ggctaaactt 1020
 attcaaaatg tatttgaat caaactacag agttttgtga aagagcagtt agaagaatgt 1080
 aggaagtccg atgcagagca atatctcaaa aatctctatg atctgtatac aagaaccacc 1140
 aatctttcca gcaagctgat ggagtttaatt ttaggtactg ataaacagac tttcttgtct 1200
 aagcttatca aatccatttt catttcctat ttggagaact atattgaggt ggagactgga 1260
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 gggagaagtg tggatacagt tttgatggaa cttggagtac gttttcatcg acttatctat 2040
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165

<210> 369
 <211> 708
 <212> PRT
 <213> Homo sapiens

<400> 369

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Tyr	Ile	Glu	Arg	Leu	Val	Trp	Arg	Thr	Pro	Gly	Gly	Gly	Ser	Arg	Gly
			20					25					30		
Gly	Pro	Glu	Ala	Phe	Asp	Pro	Lys	Arg	Leu	Leu	Glu	Glu	Phe	Val	Asn
		35					40					45			
His	Ile	Gln	Glu	Leu	Gln	Ile	Met	Asp	Glu	Arg	Ile	Gln	Arg	Lys	Val
	50					55					60				
Glu	Lys	Leu	Glu	Gln	Gln	Cys	Gln	Lys	Glu	Ala	Lys	Glu	Phe	Ala	Lys
65					70					75					80
Lys	Val	Gln	Glu	Leu	Gln	Lys	Ser	Asn	Gln	Val	Ala	Phe	Gln	His	Phe
				85					90					95	
Gln	Glu	Leu	Asp	Glu	His	Ile	Ser	Tyr	Val	Ala	Thr	Lys	Val	Cys	His
			100					105					110		
Leu	Gly	Asp	Gln	Leu	Glu	Gly	Val	Asn	Thr	Pro	Arg	Gln	Arg	Ala	Val
		115				120						125			
Glu	Ala	Gln	Lys	Leu	Met	Lys	Tyr	Phe	Asn	Glu	Phe	Leu	Asp	Gly	Glu
	130					135					140				
Leu	Lys	Ser	Asp	Val	Phe	Thr	Asn	Ser	Glu	Lys	Ile	Lys	Glu	Ala	Ala
145					150					155					160
Asp	Ile	Ile	Gln	Lys	Leu	His	Leu	Ile	Ala	Gln	Glu	Leu	Pro	Phe	Asp
			165						170					175	
Arg	Phe	Ser	Glu	Val	Lys	Ser	Lys	Ile	Ala	Ser	Lys	Tyr	His	Asp	Leu
			180					185					190		
Glu	Cys	Gln	Leu	Ile	Gln	Glu	Phe	Thr	Ser	Ala	Gln	Arg	Arg	Gly	Glu
		195					200					205			
Ile	Ser	Arg	Met	Arg	Glu	Val	Ala	Ala	Val	Leu	Leu	His	Phe	Lys	Gly
		210				215						220			
Tyr	Ser	His	Cys	Val	Asp	Val	Tyr	Ile	Lys	Gln	Cys	Gln	Glu	Gly	Ala
225					230					235					240
Tyr	Leu	Arg	Asn	Asp	Ile	Phe	Glu	Asp	Ala	Gly	Ile	Leu	Cys	Gln	Arg
			245						250					255	
Val	Asn	Lys	Gln	Val	Gly	Asp	Ile	Phe	Ser	Asn	Pro	Glu	Thr	Val	Leu
			260					265					270		
Ala	Lys	Leu	Ile	Gln	Asn	Val	Phe	Glu	Ile	Lys	Leu	Gln	Ser	Phe	Val
		275					280					285			
Lys	Glu	Gln	Leu	Glu	Glu	Cys	Arg	Lys	Ser	Asp	Ala	Glu	Gln	Tyr	Leu
		290				295					300				
Lys	Asn	Leu	Tyr	Asp	Leu	Tyr	Thr	Arg	Thr	Thr	Asn	Leu	Ser	Ser	Lys
305					310					315					320
Leu	Met	Glu	Phe	Asn	Leu	Gly	Thr	Asp	Lys	Gln	Thr	Phe	Leu	Ser	Lys
			325						330					335	
Leu	Ile	Lys	Ser	Ile	Phe	Ile	Ser	Tyr	Leu	Glu	Asn	Tyr	Ile	Glu	Val
			340					345					350		
Glu	Thr	Gly	Tyr	Leu	Lys	Ser	Arg	Ser	Ala	Met	Ile	Leu	Gln	Arg	Tyr
		355					360					365			
Tyr	Asp	Ser	Lys	Asn	His	Gln	Lys	Arg	Ser	Ile	Gly	Thr	Gly	Gly	Ile
	370					375					380				
Gln	Asp	Leu	Lys	Glu	Arg	Ile	Arg	Gln	Arg	Thr	Asn	Leu	Pro	Leu	Gly
385					390					395					400
Pro	Ser	Ile	Asp	Thr	His	Gly	Glu	Thr	Phe	Leu	Ser	Gln	Glu	Val	Val
				405					410					415	

166

Val Asn Leu Leu Gln Glu Thr Lys Gln Ala Phe Glu Arg Cys His Arg
 420 425 430
 Leu Ser Asp Pro Ser Asp Leu Pro Arg Asn Ala Phe Arg Ile Phe Thr
 435 440 445
 Ile Leu Val Glu Phe Leu Cys Ile Glu His Ile Asp Tyr Ala Leu Glu
 450 455 460
 Thr Gly Leu Ala Gly Ile Pro Ser Ser Asp Ser Arg Asn Ala Asn Leu
 465 470 475 480
 Tyr Phe Leu Asp Val Val Gln Gln Ala Asn Thr Ile Phe His Leu Phe
 485 490 495
 Asp Lys Gln Phe Asn Asp His Leu Met Pro Leu Ile Ser Ser Ser Pro
 500 505 510
 Lys Leu Ser Glu Cys Leu Gln Lys Lys Lys Glu Ile Ile Glu Gln Met
 515 520 525
 Glu Met Lys Leu Asp Thr Gly Ile Asp Arg Thr Leu Asn Cys Met Ile
 530 535 540
 Gly Gln Met Lys His Ile Leu Ala Ala Glu Gln Lys Lys Thr Asp Phe
 545 550 555 560
 Lys Pro Glu Asp Glu Asn Asn Val Leu Ile Gln Tyr Thr Asn Ala Cys
 565 570 575
 Val Lys Val Cys Ala Tyr Val Arg Lys Gln Val Glu Lys Ile Lys Asn
 580 585 590
 Ser Met Asp Gly Lys Asn Val Asp Thr Val Leu Met Glu Leu Gly Val
 595 600 605
 Arg Phe His Arg Leu Ile Tyr Glu His Leu Gln Gln Tyr Ser Tyr Ser
 610 615 620
 Cys Met Gly Gly Met Leu Ala Ile Cys Asp Val Ala Glu Tyr Arg Lys
 625 630 635 640
 Cys Ala Lys Asp Phe Lys Ile Pro Met Val Leu His Leu Phe Asp Thr
 645 650 655
 Leu His Ala Leu Cys Asn Leu Leu Val Val Ala Pro Asp Asn Leu Lys
 660 665 670
 Gln Val Cys Ser Gly Glu Gln Leu Ala Asn Leu Asp Lys Asn Ile Leu
 675 680 685
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 690 695 700
 Arg His Phe Ser
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<210> 370

<211> 60

<212> DNA

<213> Homo sapiens

<400> 370

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<210> 371

<211> 60

<212> DNA

<213> Homo sapiens

<400> 371

agtagaattt cctctggaac tggagacatt ttccagcaac atattcagct tgaaagtaca 60

<210> 372
<211> 60
<212> DNA
<213> Homo sapiens

<400> 372
ccagagactg gagatcctgt tacgctgaga ctccttgatg atggagcagg tgctgatgtt 60

<210> 373
<211> 60
<212> DNA
<213> Homo sapiens

<400> 373
ttacagtctg ctgtatctaa cattgccag gcgcctctgt ttattcccc caattctgat 60

<210> 374
<211> 60
<212> DNA
<213> Homo sapiens

<400> 374
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<210> 375
<211> 60
<212> DNA
<213> Homo sapiens

<400> 375
aaaaacacag tgactgtgga taatactgtg ggcaacgaca ctatgtttct agttacgtgg 60

<210> 376
<211> 20
<212> PRT
<213> Homo sapiens

<400> 376
Leu Gln Ser Ala Val Ser Asn Ile Ala Gln Ala Pro Leu Phe Ile Pro
1 5 10 15
Pro Asn Ser Asp
20

<210> 377
<211> 20
<212> PRT
<213> Homo sapiens

<400> 377
Val Asn His Ser Pro Ser Ile Ser Thr Pro Ala His Ser Ile Pro Gly
1 5 10 15
Ser His Ala Met
20

<210> 378
<211> 20
<212> PRT
<213> Homo sapiens

<400> 378
Pro Glu Thr Gly Asp Pro Val Thr Leu Arg Leu Leu Asp Asp Gly Ala
1 5 10 15
Gly Ala Asp Val
20

<210> 379
<211> 20
<212> PRT
<213> Homo sapiens

<400> 379
Ala Val Pro Pro Ala Thr Val Glu Ala Phe Val Glu Arg Asp Ser Leu
1 5 10 15
His Phe Pro His
20

<210> 380
<211> 20
<212> PRT
<213> Homo sapiens

<400> 380
Ser Arg Ile Ser Ser Gly Thr Gly Asp Ile Phe Gln Gln His Ile Gln
1 5 10 15
Leu Glu Ser Thr
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<210> 381
<211> 20
<212> PRT
<213> Homo sapiens

<400> 381
Lys Asn Thr Val Thr Val Asp Asn Thr Val Gly Asn Asp Thr Met Phe
1 5 10 15
Leu Val Thr Trp
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<210> 382
<211> 20
<212> PRT
<213> Homo sapiens

<400> 382
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1 5 10 15

Gln Ala Leu Lys
20

<210> 383
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 383
cggcgaattc atggattggg ggacgctgc 29

<210> 384
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 384
cggcctcgag tcacccctct atccgaacct tctgc 35

<210> 385
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 385
cggcgaattc cacgaaccac tcgcaagttc ag 32

<210> 386
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 386
cggctcgagt tagcttgggc ctgtgattgc 30

<210> 387
<211> 20
<212> PRT
<213> Homo sapiens

<400> 387
Phe Phe Lys Trp Leu Leu Ser Cys Cys Pro Gly Ser Ser Gln Ile Ala
1 5 10 15
Ala Ala Ala Ser
20

170

<210> 388
<211> 19
<212> PRT
<213> Homo sapiens

<400> 388
Leu Ser Cys Cys Pro Gly Ser Ser Gln Ile Ala Ala Ala Ser Thr Gln
1 5 10 15
Pro Glu Asp

<210> 389
<211> 20
<212> PRT
<213> Homo sapiens

<400> 389
Ala Ala Ala Ala Ser Thr Gln Pro Glu Asp Asp Ile Asn Thr Gln Arg
1 5 10 15
Lys Lys Ser Gln
20

<210> 390
<211> 20
<212> PRT
<213> Homo sapiens

<400> 390
Thr Gln Pro Glu Asp Asp Ile Asn Thr Gln Arg Lys Lys Ser Gln Glu
1 5 10 15
Lys Met Arg Glu
20

<210> 391
<211> 20
<212> PRT
<213> Homo sapiens

<400> 391
Asp Ile Asn Thr Gln Arg Lys Lys Ser Gln Glu Lys Met Arg Glu Val
1 5 10 15
Thr Asp Ser Pro
20

<210> 392
<211> 20
<212> PRT
<213> Homo sapiens

<400> 392
Arg Lys Lys Ser Gln Glu Lys Met Arg Glu Val Thr Asp Ser Pro Gly
1 5 10 15

Arg Pro Arg Glu
20

<210> 393
<211> 20
<212> PRT
<213> Homo sapiens

<400> 393
Glu Lys Met Arg Glu Val Thr Asp Ser Pro Gly Arg Pro Arg Glu Leu
1 5 10 15
Thr Ile Pro Gln
20

<210> 394
<211> 20
<212> PRT
<213> Homo sapiens

<400> 394
Val Thr Asp Ser Pro Gly Arg Pro Arg Glu Leu Thr Ile Pro Gln Thr
1 5 10 15
Ser Ser His Gly
20

<210> 395
<211> 19
<212> PRT
<213> Homo sapiens

<400> 395
Gly Arg Pro Arg Glu Leu Thr Ile Pro Gln Thr Ser Ser His Gly Ala
1 5 10 15
Asn Arg Phe

<210> 396
<211> 19
<212> PRT
<213> Homo sapiens

<400> 396
Met Asn Lys Leu Tyr Ile Gly Asn Leu Ser Glu Asn Ala Ala Pro Ser
1 5 10 15
Asp Leu Glu

<210> 397
<211> 20
<212> PRT
<213> Homo sapiens

<400> 397

172

Ser Glu Asn Ala Ala Pro Ser Asp Leu Glu Ser Ile Phe Lys Asp Ala
1 5 10 15
Lys Ile Pro Val
20

<210> 398
<211> 20
<212> PRT
<213> Homo sapiens

<400> 398
Ser Ile Phe Lys Asp Ala Lys Ile Pro Val Ser Gly Pro Phe Leu Val
1 5 10 15
Lys Thr Gly Tyr
20

<210> 399
<211> 20
<212> PRT
<213> Homo sapiens

<400> 399
Ser Gly Pro Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro
1 5 10 15
Asp Glu Ser Trp
20

<210> 400
<211> 20
<212> PRT
<213> Homo sapiens

<400> 400
Ala Phe Val Asp Cys Pro Asp Glu Ser Trp Ala Leu Lys Ala Ile Glu
1 5 10 15
Ala Leu Ser Gly
20

<210> 401
<211> 20
<212> PRT
<213> Homo sapiens

<400> 401
Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His Gly
1 5 10 15
Lys Pro Ile Glu
20

<210> 402
<211> 20
<212> PRT
<213> Homo sapiens

173

<400> 402

Lys Ile Glu Leu His Gly Lys Pro Ile Glu Val Glu His Ser Val Pro
1 5 10 15
Lys Arg Gln Arg
20

<210> 403

<211> 20

<212> PRT

<213> Homo sapiens

<400> 403

Val Glu His Ser Val Pro Lys Arg Gln Arg Ile Arg Lys Leu Gln Ile
1 5 10 15
Arg Asn Ile Pro
20

<210> 404

<211> 20

<212> PRT

<213> Homo sapiens

<400> 404

Ile Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu
1 5 10 15
Val Leu Asp Ser
20

<210> 405

<211> 20

<212> PRT

<213> Homo sapiens

<400> 405

Ala Val Val Asn Val Thr Tyr Ser Ser Lys Asp Gln Ala Arg Gln Ala
1 5 10 15
Leu Asp Lys Leu
20

<210> 406

<211> 20

<212> PRT

<213> Homo sapiens

<400> 406

Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu Glu
1 5 10 15
Asn Phe Thr Leu
20

<210> 407

<211> 20

Asn Gly Phe Gln Leu Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro
1 5 10 15
Asp Glu Thr Ala
20

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<210> 408
<211> 20
<212> PRT
<213> Homo sapiens
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Lys Val Ala Tyr Ile Pro Asp Glu Thr Ala Ala Gln Gln Asn Pro Leu
1 5 10 15
Gln Gln Pro Arg
20

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<210> 409
<211> 20
<212> PRT
<213> Homo sapiens
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Ala Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly
1 5 10 15
Gln Arg Gly Ser
20

```
<210> 410
<211> 20
<212> PRT
<213> Homo sapiens
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Gly Arg Arg Gly Leu Gly Gln Arg Gly Ser Ser Arg Gln Gly Ser Pro
1 5 10 15
Gly Ser Val Ser
20

```
<210> 411
<211> 20
<212> PRT
<213> Homo sapiens
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Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys Pro Cys Asp
1 5 10 15
Leu Pro Leu Arg
20

175

<210> 412
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 412
 Lys Gln Lys Pro Cys Asp Leu Pro Leu Arg Leu Leu Val Pro Thr Gln
 1 5 10 15
 Phe Val Gly Ala
 20

<210> 413
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 413
 Leu Leu Val Pro Thr Gln Phe Val Gly Ala Ile Ile Gly Lys Glu Gly
 1 5 10 15
 Ala Thr Ile Arg
 20

<210> 414
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 414
 Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln Thr
 1 5 10 15
 Gln Ser Lys Ile
 20

<210> 415
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 415
 Asn Ile Thr Lys Gln Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu
 1 5 10 15
 Asn Ala Gly Ala
 20

<210> 416
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 416
 Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala Glu Lys Ser Ile Thr
 1 5 10 15
 Ile Leu Ser Thr
 20

176

<210> 417
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 417
 Ala Glu Lys Ser Ile Thr Ile Leu Ser Thr Pro Glu Gly Thr Ser Ala
 1 5 10 15
 Ala Cys Lys Ser
 20

<210> 418
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 418
 Pro Glu Gly Thr Ser Ala Ala Cys Lys Ser Ile Leu Glu Ile Met His
 1 5 10 15
 Lys Glu Ala Gln
 20

<210> 419
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 419
 Ile Leu Glu Ile Met His Lys Glu Ala Gln Asp Ile Lys Phe Thr Glu
 1 5 10 15
 Glu Ile Pro Leu
 20

<210> 420
 <211> 455
 <212> DNA
 <213> Homo sapiens

<400> 420
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 gccctagcca acgccgcatg agagggagtg tgccgagggc ttctgagaag gtttctctca 120
 catctagaaa gaagcgctta agatgtggca gcccctcttc ttcaagtggc tcttgtcctg 180
 ttgccctggg agttctcaaa ttgctgcagc agcctccacc cagcctgagg atgacatcaa 240
 tacacagagg aagaagagtc aggaaaagat gagagaagtt acagactctc ctgggcgacc 300
 ccgagagctt accatttctc agacttcttc acatggtgct aacagatttg ttcctaaaag 360
 taaagctcta gagggcgtca aattggcaat agaagccggg ttccaccata ttgattctgc 420
 acatgtttac aataatgagg agcaggttgg actgg 455

<210> 421
 <211> 24
 <212> DNA
 <213> Artificial Sequence

177

<220>

<223> PCR primer

<400> 421

actagtgtcc gcgtggcggc ctac

24

<210> 422

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 422

catgagaatt catcacatgc ccttgaaggc tccc

34

<210> 423

<211> 161

<212> PRT

<213> Homo sapiens

<400> 423

Met	Gln	His	His	His	His	His	His	His	Thr	Ser	Val	Arg	Val	Ala	Ala
1				5					10					15	
Tyr	Phe	Glu	Asn	Phe	Leu	Ala	Ala	Trp	Arg	Pro	Val	Lys	Ala	Ser	Asp
			20					25					30		
Gly	Asp	Tyr	Tyr	Thr	Leu	Ala	Val	Pro	Met	Gly	Asp	Val	Pro	Met	Asp
		35					40					45			
Gly	Ile	Ser	Val	Ala	Asp	Ile	Gly	Ala	Ala	Val	Ser	Ser	Ile	Phe	Asn
	50					55					60				
Ser	Pro	Glu	Glu	Phe	Leu	Gly	Lys	Ala	Val	Gly	Leu	Ser	Ala	Glu	Ala
65					70					75				80	
Leu	Thr	Ile	Gln	Gln	Tyr	Ala	Asp	Val	Leu	Ser	Lys	Ala	Leu	Gly	Lys
			85					90					95		
Glu	Val	Arg	Asp	Ala	Lys	Ile	Thr	Pro	Glu	Ala	Phe	Glu	Lys	Leu	Gly
			100					105					110		
Phe	Pro	Ala	Ala	Lys	Glu	Ile	Ala	Asn	Met	Cys	Arg	Phe	Tyr	Glu	Met
			115				120					125			
Lys	Pro	Asp	Arg	Asp	Val	Asn	Leu	Thr	His	Gln	Leu	Asn	Pro	Lys	Val
	130					135					140				
Lys	Ser	Phe	Ser	Gln	Phe	Ile	Ser	Glu	Asn	Gln	Gly	Ala	Phe	Lys	Gly
145					150					155					160
Met															

<210> 424

<211> 489

<212> DNA

<213> Homo sapiens

<400> 424

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 tttctcgcg cgtggcggcc cgtgaaagcc tctgatggag attactacac cttggctgta 120
 ccgatgggag atgtaccaat ggatgtatc tctgttgctg atattggagc agccgtctct 180
 agcattttta attctccaga ggaattttta ggcaaggccg tggggctcag tgcagaagca 240
 ctaacaatac agcaatatgc tgatgttttg tccaaggctt tggggaaaga agtccgagat 300

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<210> 425
<211> 32
<212> DNA
<213> Artificial Sequence
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<220>
<223> PCR primer

<400> 425
aacaaactgt atatcgaaa cctcagcgag aa 32

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<210> 426
<211> 33
<212> DNA
<213> Artificial Sequence
```

<220>
<223> PCR primer

<400> 426
ccatagaatt cattacttcc gtcttgactg agg 33

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<210> 427
<211> 586
<212> PRT
<213> Homo sapiens
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<400> 427																
Met 1	Gln	His	His	His	His	His	His	Asn	Lys	Leu	Tyr	Ile	Gly	Asn	Leu	
				5				10						15		
Ser	Glu	Asn	Ala	Ala	Pro	Ser	Asp	Leu	Glu	Ser	Ile	Phe	Lys	Asp	Ala	
			20					25					30			
Lys	Ile	Pro	Val	Ser	Gly	Pro	Phe	Leu	Val	Lys	Thr	Gly	Tyr	Ala	Phe	
		35				40						45				
Val	Asp	Cys	Pro	Asp	Glu	Ser	Trp	Ala	Leu	Lys	Ala	Ile	Glu	Ala	Leu	
	50					55					60					
Ser	Gly	Lys	Ile	Glu	Leu	His	Gly	Lys	Pro	Ile	Glu	Val	Glu	His	Ser	
65				70					75						80	
Val	Pro	Lys	Arg	Gln	Arg	Ile	Arg	Lys	Leu	Gln	Ile	Arg	Asn	Ile	Pro	
				85					90					95		
Pro	His	Leu	Gln	Trp	Glu	Val	Leu	Asp	Ser	Leu	Leu	Val	Gln	Tyr	Gly	
			100					105					110			
Val	Val	Glu	Ser	Cys	Glu	Gln	Val	Asn	Thr	Asp	Ser	Glu	Thr	Ala	Val	
		115				120						125				
Val	Asn	Val	Thr	Tyr	Ser	Ser	Lys	Asp	Gln	Ala	Arg	Gln	Ala	Leu	Asp	
	130					135					140					
Lys	Leu	Asn	Gly	Phe	Gln	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Val	Ala	Tyr	
145				150					155					160		
Ile	Pro	Asp	Glu	Thr	Ala	Ala	Gln	Gln	Asn	Pro	Leu	Gln	Gln	Pro	Arg	
			165						170					175		
Gly	Arg	Arg	Gly	Leu	Gly	Gln	Arg	Gly	Ser	Ser	Arg	Gln	Gly	Ser	Pro	
		180						185					190			
Gly	Ser	Val	Ser	Lys	Gln	Lys	Pro	Cys	Asp	Leu	Pro	Leu	Arg	Leu	Leu	

195	200	205
Val Pro Thr Gln Phe Val Gly Ala Ile Ile Gly Lys Glu Gly Ala Thr		
210	215	220
Ile Arg Asn Ile Thr Lys Gln Thr Gln Ser Lys Ile Asp Val His Arg		
225	230	235
Lys Glu Asn Ala Gly Ala Ala Glu Lys Ser Ile Thr Ile Leu Ser Thr		
245	250	255
Pro Glu Gly Thr Ser Ala Ala Cys Lys Ser Ile Leu Glu Ile Met His		
260	265	270
Lys Glu Ala Gln Asp Ile Lys Phe Thr Glu Glu Ile Pro Leu Lys Ile		
275	280	285
Leu Ala His Asn Asn Phe Val Gly Arg Leu Ile Gly Lys Glu Gly Arg		
290	295	300
Asn Leu Lys Lys Ile Glu Gln Asp Thr Asp Thr Lys Ile Thr Ile Ser		
305	310	315
Pro Leu Gln Glu Leu Thr Leu Tyr Asn Pro Glu Arg Thr Ile Thr Val		
325	330	335
Lys Gly Asn Val Glu Thr Cys Ala Lys Ala Glu Glu Glu Ile Met Lys		
340	345	350
Lys Ile Arg Glu Ser Tyr Glu Asn Asp Ile Ala Ser Met Asn Leu Gln		
355	360	365
Ala His Leu Ile Pro Gly Leu Asn Leu Asn Ala Leu Gly Leu Phe Pro		
370	375	380
Pro Thr Ser Gly Met Pro Pro Pro Thr Ser Gly Pro Pro Ser Ala Met		
385	390	395
Thr Pro Pro Tyr Pro Gln Phe Glu Gln Ser Glu Thr Glu Thr Val His		
405	410	415
Leu Phe Ile Pro Ala Leu Ser Val Gly Ala Ile Ile Gly Lys Gln Gly		
420	425	430
Gln His Ile Lys Gln Leu Ser Arg Phe Ala Gly Ala Ser Ile Lys Ile		
435	440	445
Ala Pro Ala Glu Ala Pro Asp Ala Lys Val Arg Met Val Ile Ile Thr		
450	455	460
Gly Pro Pro Glu Ala Gln Phe Lys Ala Gln Gly Arg Ile Tyr Gly Lys		
465	470	475
Ile Lys Glu Glu Asn Phe Val Ser Pro Lys Glu Glu Val Lys Leu Glu		
485	490	495
Ala His Ile Arg Val Pro Ser Phe Ala Ala Gly Arg Val Ile Gly Lys		
500	505	510
Gly Gly Lys Thr Val Asn Glu Leu Gln Asn Leu Ser Ser Ala Glu Val		
515	520	525
Val Val Pro Arg Asp Gln Thr Pro Asp Glu Asn Asp Gln Val Val Val		
530	535	540
Lys Ile Thr Gly His Phe Tyr Ala Cys Gln Val Ala Gln Arg Lys Ile		
545	550	555
Gln Glu Ile Leu Thr Gln Val Lys Gln His Gln Gln Gln Lys Ala Leu		
565	570	575
Gln Ser Gly Pro Gln Ser Arg Arg Lys		
580	585	

<210> 428

<211> 1764

<212> DNA

<213> Homo sapiens

<400> 428

atgcagcatc accaccatca ccacaacaaa ctgtatatcg gaaacctcag cgagaacgcc 60

180

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gccccctcgg acctagaaaag tatcttcaag gacgccaaga tcccgggtgtc gggacccttc 120
ctggtgaaga ctggctacgc gttcgtggac tgcccggacg agagctgggc cctcaaggcc 180
atcgaggcgc tttcaggtaa aatagaactg caccggaaac ccatagaagt tgagcactcg 240
gtoccaaaaa ggcaaaggat tcggaaactt cagatacgaa atatcccgcc tcatttacag 300
tgggaggtgc tggatagttt actagtccag tatggagtgg tggagagctg tgagcaagtg 360
aacactgact cggaaactgc agttgtaaat gtaacctatt ccagtaagga ccaagctaga 420
caagcactag acaaactgaa tggatttcag ttagagaatt tcaccttgaa agtagcctat 480
atccctgatg aaacggccgc ccagcaaaac cccttgacgc agccccgagg tcgccggggg 540
cttgggcaga ggggctcctc aaggcagggg tctccaggat ccgtatccaa gcagaaacca 600
tgtgatttgc ctctgcgcct gctgggtccc acccaatttg ttggagccat cataggaaaa 660
gaaggtgcc aatttcgga catcaccaaa cagaccaggt ctaaaatcga tgtccaccgt 720
aaagaaaatg cgggggctgc tgagaagtgc attactatcc tctctactcc tgaaggcacc 780
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acagaagaga tccccttgaa gatttttagct cataataact ttgttgagcg tcttatttgt 900
aaagaaggaa gaaatcttaa aaaaattgag caagacacag aactaaaaat cactgatctc 960
ccattgcagg aattgacgct gtataatcca gaacgcacta ttacagttaa aggcaatgtt 1020
gagacatgtg ccaaagctga ggaggagatc atgaagaaaa tcagggagtc ttatgaaaa 1080
gatattgctt ctatgaatct tcaagcacat ttaattcctg gattaaatct gaacgccttg 1140
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actcctccct acccgagctt tgagcaatca gaaacggaga ctgttcatct gtttatcca 1260
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gtgccatcct ttgctgctgg cagagttatt ggaaaaggag gcaaaacggt gaatgaactt 1560
cagaatttgt caagtgcaga agttgtgtgc cctcgtgacc agacacctga tgagaatgac 1620
caagtgggtg tcaaaataac tggtcacttc tatgcttgcc aggttgccca gagaaaaatt 1680
caggaaattc tgactcaggt aaagcagcac caacaacaga aggctctgca aagtggacca 1740
cctcagtcaa gacggaagta atga 1764

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<210> 429

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 429.

ccatggaatt cattatttca atataagata atctc

35

<210> 430

<211> 881

<212> PRT

<213> Homo sapiens

<400> 430

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Met Gln His His His His His Gly Val Gln Leu Gln Asp Asn Gly
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Tyr Asn Gly Leu Leu Ile Ala Ile Asn Pro Gln Val Pro Glu Asn Gln
          20          25          30
Asn Leu Ile Ser Asn Ile Lys Glu Met Ile Thr Glu Ala Ser Phe Tyr
          35          40          45
Leu Phe Asn Ala Thr Lys Arg Arg Val Phe Phe Arg Asn Ile Lys Ile
          50          55          60
Leu Ile Pro Ala Thr Trp Lys Ala Asn Asn Asn Ser Lys Ile Lys Gln
          65          70          75          80
Glu Ser Tyr Glu Lys Ala Asn Val Ile Val Thr Asp Trp Tyr Gly Ala

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545 550 555 560
 His Ser Leu Gln Ala Leu Lys Val Thr Val Thr Ser Arg Ala Ser Asn
 565 570 575
 Ser Ala Val Pro Pro Ala Thr Val Glu Ala Phe Val Glu Arg Asp Ser
 580 585 590
 Leu His Phe Pro His Pro Val Met Ile Tyr Ala Asn Val Lys Gln Gly
 595 600 605
 Phe Tyr Pro Ile Leu Asn Ala Thr Val Thr Ala Thr Val Glu Pro Glu
 610 615 620
 Thr Gly Asp Pro Val Thr Leu Arg Leu Leu Asp Asp Gly Ala Gly Ala
 625 630 635 640
 Asp Val Ile Lys Asn Asp Gly Ile Tyr Ser Arg Tyr Phe Phe Ser Phe
 645 650 655
 Ala Ala Asn Gly Arg Tyr Ser Leu Lys Val His Val Asn His Ser Pro
 660 665 670
 Ser Ile Ser Thr Pro Ala His Ser Ile Pro Gly Ser His Ala Met Tyr
 675 680 685
 Val Pro Gly Tyr Thr Ala Asn Gly Asn Ile Gln Met Asn Ala Pro Arg
 690 695 700
 Lys Ser Val Gly Arg Asn Glu Glu Glu Arg Lys Trp Gly Phe Ser Arg
 705 710 715 720
 Val Ser Ser Gly Gly Ser Phe Ser Val Leu Gly Val Pro Ala Gly Pro
 725 730 735
 His Pro Asp Val Phe Pro Pro Cys Lys Ile Ile Asp Leu Glu Ala Val
 740 745 750
 Lys Val Glu Glu Glu Leu Thr Leu Ser Trp Thr Ala Pro Gly Glu Asp
 755 760 765
 Phe Asp Gln Gly Gln Ala Thr Ser Tyr Glu Ile Arg Met Ser Lys Ser
 770 775 780
 Leu Gln Asn Ile Gln Asp Asp Phe Asn Asn Ala Ile Leu Val Asn Thr
 785 790 795 800
 Ser Lys Arg Asn Pro Gln Gln Ala Gly Ile Arg Glu Ile Phe Thr Phe
 805 810 815
 Ser Pro Gln Ile Ser Thr Asn Gly Pro Glu His Gln Pro Asn Gly Glu
 820 825 830
 Thr His Glu Ser His Arg Ile Tyr Val Ala Ile Arg Ala Met Asp Arg
 835 840 845
 Asn Ser Leu Gln Ser Ala Val Ser Asn Ile Ala Gln Ala Pro Leu Phe
 850 855 860
 Ile Pro Pro Asn Ser Asp Pro Val Pro Ala Arg Asp Tyr Leu Ile Leu
 865 870 875 880
 Lys

<210> 431

<211> 2646

<212> DNA

<213> Homo sapiens

<400> 431

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 atgataactg aagcttcatt ttacctatit aatgctacca agagaagagt atttttcaga 180
 aatataaaga ttttaatacc tgccacatgg aaagctaata ataacagcaa aataaaacaa 240
 gaatcatatg aaaaggcaaa tgatcatagt actgactggt atggggcaca tggagatgat 300
 ccatacacc tacaatacag aggggtgtgga aaagagggaa aatacattca tttcacacct 360
 aatttcctac tgaatgataa cttaacagct ggctacggat cagaggccg agtgtttgtc 420

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catgaatggg cccacctccg ttggggtgtg ttcgatgagt ataacaatga caaacctttc 480
tacataaatg ggcaaaatca aattaaagtg acaagggtgtt catctgacat cacaggcatt 540
tttgtgtgtg aaaaagggtcc ttgcccccaa gaaaactgta ttattagtaa gcttttttaa 600
gaaggatgca cctttatcta caatagcacc caaaatgcaa ctgcatcaat aatgttcatt 660
caaagtttat cttctgtgtg tgaattttgt aatgcaagta cccacaacca agaagcacca 720
aacctacaga accagatgtg cagcctcaga agtgcatggg atgtaatcac agactctgct 780
gactttcacc acagctttcc catgaacggg actgagcttc cacctcctcc cacattctcg 840
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gaggctgaca gactccttca actacaacaa gccgcagaat tttatttgat gcagattgtt 960
gaaattcata ccttcgtggg cattgccagt ttcgacagca aaggagagat cagagcccag 1020
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gttgagccag agactggaga tctgtttacg ctgagactcc ttgatgatgg agcagggtct 1920
gatgttataa aaaatgatgg aattttactc aggtattttt tctcctttgc tgcaaatggt 1980
agatatagct tgaaagtgca tgtcaatcac tctccagca taagcaccac agccactct 2040
attccaggga gtcatgctat gtatgtacca ggttacacag caaacggtaa tattcagatg 2100
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gttgcaatac gagcaatgga taggaactcc ttacagtctg ctgtatctaa cattgccag 2580
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<210> 432

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 432

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36

<210> 433

<211> 371

<212> PRT

<213> Homo sapiens

<400> 433

Met Gln His His His His His Trp Gln Pro Leu Phe Phe Lys Trp

1

5

10

15

184

Leu Leu Ser Cys Cys Pro Gly Ser Ser Gln Ile Ala Ala Ala Ala Ser
 20 25 30
 Thr Gln Pro Glu Asp Asp Ile Asn Thr Gln Arg Lys Lys Ser Gln Glu
 35 40 45
 Lys Met Arg Glu Val Thr Asp Ser Pro Gly Arg Pro Arg Glu Leu Thr
 50 55 60
 Ile Pro Gln Thr Ser Ser His Gly Ala Asn Arg Phe Val Pro Lys Ser
 65 70 75 80
 Lys Ala Leu Glu Ala Val Lys Leu Ala Ile Glu Ala Gly Phe His His
 85 90 95
 Ile Asp Ser Ala His Val Tyr Asn Asn Glu Glu Gln Val Gly Leu Ala
 100 105 110
 Ile Arg Ser Lys Ile Ala Asp Gly Ser Val Lys Arg Glu Asp Ile Phe
 115 120 125
 Tyr Thr Ser Lys Leu Trp Ser Asn Ser His Arg Pro Glu Leu Val Arg
 130 135 140
 Pro Ala Leu Glu Arg Ser Leu Lys Asn Leu Gln Leu Asp Tyr Val Asp
 145 150 155 160
 Leu Tyr Leu Ile His Phe Pro Val Ser Val Lys Pro Gly Glu Glu Val
 165 170 175
 Ile Pro Lys Asp Glu Asn Gly Lys Ile Leu Phe Asp Thr Val Asp Leu
 180 185 190
 Cys Ala Thr Trp Glu Ala Met Glu Lys Cys Lys Asp Ala Gly Leu Ala
 195 200 205
 Lys Ser Ile Gly Val Ser Asn Phe Asn His Arg Leu Leu Glu Met Ile
 210 215 220
 Leu Asn Lys Pro Gly Leu Lys Tyr Lys Pro Val Cys Asn Gln Val Glu
 225 230 235 240
 Cys His Pro Tyr Phe Asn Gln Arg Lys Leu Leu Asp Phe Cys Lys Ser
 245 250 255
 Lys Asp Ile Val Leu Val Ala Tyr Ser Ala Leu Gly Ser His Arg Glu
 260 265 270
 Glu Pro Trp Val Asp Pro Asn Ser Pro Val Leu Leu Glu Asp Pro Val
 275 280 285
 Leu Cys Ala Leu Ala Lys Lys His Lys Arg Thr Pro Ala Leu Ile Ala
 290 295 300
 Leu Arg Tyr Gln Leu Gln Arg Gly Val Val Val Leu Ala Lys Ser Tyr
 305 310 315 320
 Asn Glu Gln Arg Ile Arg Gln Asn Val Gln Val Phe Glu Phe Gln Leu
 325 330 335
 Thr Ser Glu Glu Met Lys Ala Ile Asp Gly Leu Asn Arg Asn Val Arg
 340 345 350
 Tyr Leu Thr Leu Asp Ile Phe Ala Gly Pro Pro Asn Tyr Pro Phe Ser
 355 360 365
 Asp Glu Tyr
 370

<210> 434

<211> 1119

<212> DNA

<213> Homo sapiens

<400> 434

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acacagagga agaagagtcg ggaagagatg agagaagtta cagactctcc tgggcgaccc	180
cgagagctta ccattcctca gacttcttca catggtgcta acagatttgt tcctaaaagt	240

aaagctctag	aggccgtcaa	attggcaata	gaagccgggt	tccaccatat	tgattctgca	300
catgtttaca	ataatgagga	gcaggttgga	ctggccatcc	gaagcaagat	tgcatatggc	360
agtgtgaaga	gagaagacat	attctacact	tcaaagcttt	ggagcaattc	ccatcgacca	420
gagttggtcc	gaccagcctt	ggaaagggtca	ctgaaaaatc	ttcaattgga	ctatgttgac	480
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gaaaatggaa	aaatactatt	tgacacagtg	gatctctgtg	ccacatggga	ggccatggag	600
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gccctgattg	ccctgcgcta	ccagctgcag	cgtgggggtg	tggtcctggc	caagagctac	960
aatgagcagc	gcacagaca	gaacgtgcag	gtgtttgaat	tccagttgac	ttcagaggag	1020
atgaaagcca	tagatggcct	aaacagaaat	gtgcgatatt	tgacccttga	tatttttgct	1080
ggcccccccta	attatccatt	ttctgatgaa	tattaatga			1119

<210> 435

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 435

ggatccgccg ccaccatgac atccattcga gctgta 36

<210> 436

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 436

gtcgactcag ctggaccaca gccgcag 27

<210> 437

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 437

ggatccgccg ccaccatgga ctcttgacc ttctgct 37

<210> 438

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 438

gtcgactcag aaatcctttc tcttgac

27

<210> 439

<211> 933

<212> DNA

<213> Homo sapiens

<400> 439

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agatgtaaac	caatttcagg	acacgactac	cttttctggg	acagacagac	catgatgcgg	180
ggactggagt	tgctcattta	ctttaacaac	aacgttccga	tagatgattc	agggatgccc	240
gaggatcgat	tctcagctaa	gatgcctaata	gcatcattct	ccactctgaa	gatccagccc	300
tcagaaccca	gggactcagc	tgtgtacttc	tgtgccagca	gtttagtggg	agcaaact	360
gaagctttct	ttggacaagg	caccagactc	acagttgtag	aggacctgaa	caaggtgttc	420
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acactgggtg	gcctggccac	aggcttcttc	cctgaccacg	tggagctgag	ctgggtgggtg	540
aatgggaagg	aggtgcacag	tggggtcagc	acggaccgcg	agcccctcaa	ggagcagccc	600
gccctcaatg	actccagata	ctgcctgagc	agccgcctga	gggtctcggc	caccttctgg	660
cagaaccccc	gcaaccactt	ccgctgtcaa	gtccagttct	acgggctctc	ggagaatgac	720
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agagcagact	gtggctttac	ctcggtgtcc	taccagcaag	gggtcctgtc	tgccaccatc	840
ctctatgaga	tcctgctagg	gaaggccacc	ctgtatgctg	tgctgggtcag	cgcccttggtg	900
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<210> 440

<211> 822

<212> DNA

<213> Homo sapiens

<400> 440

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gagaatgtgg	agcagcatcc	ttcaaccctg	agtgtccagg	agggagacag	cgctgttatc	120
aagtgtactt	attcagacag	tgctcaaac	tacttccctt	ggtataagca	agaacttggg	180
aaaagacctc	agcttattat	agacattcgt	tcaaatgtgg	gcgaaaagaa	agaccaacga	240
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cttgaagact	cggctgtcta	cttctgtgca	gcaagtatac	tgaacaccgg	taaccagttc	360
tattttggga	cagggacaag	tttgacggtc	attccaaata	tccagaacct	tgacctgcc	420
gtgtaccagc	tgagagactc	taaatccagt	gacaagtctg	tctgcctatt	caccgatttt	480
gattctcaaa	caaatgtgtc	acaaagtaag	gattctgatg	tgtatatcac	agacaaaact	540
gtgctagaca	tgaggtctat	ggacttcaag	agcaacagtg	ctgtggcctg	gagcaacaaa	600
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cccagcccag	aaagttcctg	tgatgtcaag	ctggtcgaga	aaagctttga	aacagatacg	720
aacctaaact	ttcaaaacct	gtcagtgatt	gggttccgaa	tcctcctcct	gaaagtggcc	780
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<210> 441

<211> 2311

<212> DNA

<213> Homo sapiens

<400> 441

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gtctccctgt	tctgtcctag	ctatgttctt	gtgttggtg	cattcgtctt	ttccagagca	180
aaccgcccag	agtagaagat	ggattggggc	acgtctcaga	cgatcctggg	gggtgtgaac	240
aaacactcca	ccagcattgg	aaagatctgg	ctcaccgtcc	tcttcatttt	tcgcattatg	300

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atcctcggtg tggctgcaaa ggaggtgtgg ggagatgagc aggccgactt tgtctgcaac 360
accctgcagc caggctgcaa gaacgtgtgc tacgatcact acttccccat ctccacatc 420
cggctatggg ccctgcagct gatcttcgtg tccagcccag cgctcctagt ggccatgcac 480
gtggcctacc ggagacatga gaagaagagg aagttcatca agggggagat aaagagtga 540
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cccaacactg tggactgctt tgtgtcccgg ccacgggaga agactgtctt cacagtgttc 780
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cagcatcgga aagaacgctg atttaaagag gtgagcttgg gaattttatt gacacagtac 1860
catttaatgg ggagacaaaa atgggggcca ggggaggag aagtttctgt cgttaaaaac 1920
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tcagtggagg taagtatttt cctgttgtca agaatagcat tgtaaaagca ttttgtaata 2220
ataaagaata gctttaatga tatgcttgta actaaaataa ttttgtaatg tatcaaatc 2280
atttaaaaca ttaaaatata atctctataa t 2311

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<210> 442

<211> 226

<212> PRT

<213> Homo sapiens

<400> 442

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Met Asp Trp Gly Thr Leu Gln Thr Ile Leu Gly Gly Val Asn Lys His
          5              10              15

```

```

Ser Thr Ser Ile Gly Lys Ile Trp Leu Thr Val Leu Phe Ile Phe Arg
          20              25              30

```

```

Ile Met Ile Leu Val Val Ala Ala Lys Glu Val Trp Gly Asp Glu Gln
          35              40              45

```

```

Ala Asp Phe Val Cys Asn Thr Leu Gln Pro Gly Cys Lys Asn Val Cys
          50              55              60

```

```

Tyr Asp His Tyr Phe Pro Ile Ser His Ile Arg Leu Trp Ala Leu Gln
          65              70              75              80

```

```

Leu Ile Phe Val Ser Ser Pro Ala Leu Leu Val Ala Met His Val Ala
          85              90              95

```

188

Tyr Arg Arg His Glu Lys Lys Arg Lys Phe Ile Lys Gly Glu Ile Lys
 100 105 110
 Ser Glu Phe Lys Asp Ile Glu Glu Ile Lys Thr Gln Lys Val Arg Ile
 115 120 125
 Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser Ile Phe Phe Arg Val
 130 135 140
 Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr Val Met Tyr Asp Gly
 145 150 155 160
 Phe Ser Met Gln Arg Leu Val Lys Cys Asn Ala Trp Pro Cys Pro Asn
 165 170 175
 Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu Lys Thr Val Phe Thr
 180 185 190
 Val Phe Met Ile Ala Val Ser Gly Ile Cys Ile Leu Leu Asn Val Thr
 195 200 205
 Glu Leu Cys Tyr Leu Leu Ile Arg Tyr Cys Ser Gly Lys Ser Lys Lys
 210 215 220
 Pro Val
 225

<210> 443
 <211> 23
 <212> PRT
 <213> Homo sapiens

<400> 443
 Val Lys Leu Cys Gly Ile Asp Pro Cys Pro Asn Leu Val Asp Cys Phe
 5 10 15
 Ile Ser Arg Pro Gly Cys Gly
 20

<210> 444
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 444
 caatcaggca tgcacaacaa actgtatatc ggaaac

36

<210> 445
 <211> 30
 <212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 445

cgtcaagatc ttcattactt ccgtcttgac

30

<210> 446

<211> 579

<212> PRT

<213> Homo sapiens

<400> 446

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Met Asn Lys Leu Tyr Ile Gly Asn Leu Ser Glu Asn Ala Ala Pro Ser
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Asp Leu Glu Ser Ile Phe Lys Asp Ala Lys Ile Pro Val Ser Gly Pro
      20              25              30

Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
      35              40              45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
      50              55              60

Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile
      65              70              75              80

Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
      85              90              95

Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln
      100             105             110

Val Asn Thr Asp Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Ser
      115             120             125

Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu
      130             135             140

Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Thr Ala Ala
      145             150             155             160

Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln
      165             170             175

Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys
      180             185             190

Pro Cys Asp Leu Pro Leu Arg Leu Leu Val Pro Thr Gln Phe Val Gly
      195             200             205

Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
      210             215             220

Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
      225             230             235             240

```

190

Glu Lys Ser Ile Thr Ile Leu Ser Thr Pro Glu Gly Thr Ser Ala Ala
 245 250 255
 Cys Lys Ser Ile Leu Glu Ile Met His Lys Glu Ala Gln Asp Ile Lys
 260 265 270
 Phe Thr Glu Glu Ile Pro Leu Lys Ile Leu Ala His Asn Asn Phe Val
 275 280 285
 Gly Arg Leu Ile Gly Lys Glu Gly Arg Asn Leu Lys Lys Ile Glu Gln
 290 295 300
 Asp Thr Asp Thr Lys Ile Thr Ile Ser Pro Leu Gln Glu Leu Thr Leu
 305 310 315 320
 Tyr Asn Pro Glu Arg Thr Ile Thr Val Lys Gly Asn Val Glu Thr Cys
 325 330 335
 Ala Lys Ala Glu Glu Glu Ile Met Lys Lys Ile Arg Glu Ser Tyr Glu
 340 345 350
 Asn Asp Ile Ala Ser Met Asn Leu Gln Ala His Leu Ile Pro Gly Leu
 355 360 365
 Asn Leu Asn Ala Leu Gly Leu Phe Pro Pro Thr Ser Gly Met Pro Pro
 370 375 380
 Pro Thr Ser Gly Pro Pro Ser Ala Met Thr Pro Pro Tyr Pro Gln Phe
 385 390 395 400
 Glu Gln Ser Glu Thr Glu Thr Val His Leu Phe Ile Pro Ala Leu Ser
 405 410 415
 Val Gly Ala Ile Ile Gly Lys Gln Gly Gln His Ile Lys Gln Leu Ser
 420 425 430
 Arg Phe Ala Gly Ala Ser Ile Lys Ile Ala Pro Ala Glu Ala Pro Asp
 435 440 445
 Ala Lys Val Arg Met Val Ile Ile Thr Gly Pro Pro Glu Ala Gln Phe
 450 455 460
 Lys Ala Gln Gly Arg Ile Tyr Gly Lys Ile Lys Glu Glu Asn Phe Val
 465 470 475 480
 Ser Pro Lys Glu Glu Val Lys Leu Glu Ala His Ile Arg Val Pro Ser
 485 490 495
 Phe Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu
 500 505 510
 Leu Gln Asn Leu Ser Ser Ala Glu Val Val Val Pro Arg Asp Gln Thr
 515 520 525
 Pro Asp Glu Asn Asp Gln Val Val Val Lys Ile Thr Gly His Phe Tyr
 530 535 540
 Ala Cys Gln Val Ala Gln Arg Lys Ile Gln Glu Ile Leu Thr Gln Val

191

545 550 555 560

Lys Gln His Gln Gln Gln Lys Ala Leu Gln Ser Gly Pro Pro Gln Ser

 565 570 575

Arg Arg Lys

<210> 447
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 447

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cggaaacttc	agatacgaaa	tatcccgctc	catttacagt	gggaggtgct	ggatagttta	300
ctagtccagt	atggagtggt	ggagagctgt	gagcaagtga	acactgactc	ggaaactgca	360
gttgtaaatg	taacctattc	cagtaaggac	caagctagac	aagcactaga	caaactgaat	420
ggatttcagt	tagagaattt	caccttgaaa	gtagcctata	tccctgatga	aacggccgcc	480
cagcaaaacc	ccttgacgca	gccccgaggt	cgccgggggc	ttgggcagag	gggctcctca	540
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<210> 448
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 448
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192

<210> 449

<211> 579

<212> PRT

<213> Homo sapiens

<400> 449

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Met Asn Lys Leu Tyr Ile Gly Asn Leu Ser Glu Asn Ala Ala Pro Ser
      5              10              15

Asp Leu Glu Ser Ile Phe Lys Asp Ala Lys Ile Pro Val Ser Gly Pro
      20              25              30

Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
      35              40              45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
      50              55              60

Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile
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Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
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Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln
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Val Asn Thr Asp Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Ser
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Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu
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Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Thr Ala Ala
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Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln
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Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys
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Pro Cys Asp Leu Pro Leu Arg Leu Leu Val Pro Thr Gln Phe Val Gly
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Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
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Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
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Glu Lys Ser Ile Thr Ile Leu Ser Thr Pro Glu Gly Thr Ser Ala Ala
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Cys Lys Ser Ile Leu Glu Ile Met His Lys Glu Ala Gln Asp Ile Lys
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Phe Thr Glu Glu Ile Pro Leu Lys Ile Leu Ala His Asn Asn Phe Val

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Tyr	Asn	Pro	Glu	Arg	Thr	Ile	Thr	Val	Lys	Gly	Asn	Val	Glu	Thr	Cys
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Asn	Leu	Asn	Ala	Leu	Gly	Leu	Phe	Pro	Pro	Thr	Ser	Gly	Met	Pro	Pro
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Val	Gly	Ala	Ile	Ile	Gly	Lys	Gln	Gly	Gln	His	Ile	Lys	Gln	Leu	Ser
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Ala	Lys	Val	Arg	Met	Val	Ile	Ile	Thr	Gly	Pro	Pro	Glu	Ala	Gln	Phe
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Lys	Ala	Gln	Gly	Arg	Ile	Tyr	Gly	Lys	Ile	Lys	Glu	Glu	Asn	Phe	Val
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Phe	Ala	Ala	Gly	Arg	Val	Ile	Gly	Lys	Gly	Gly	Lys	Thr	Val	Asn	Glu
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Leu	Gln	Asn	Leu	Ser	Ser	Ala	Glu	Val	Val	Val	Pro	Arg	Asp	Gln	Thr
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Pro	Asp	Glu	Asn	Asp	Gln	Val	Val	Val	Lys	Ile	Thr	Gly	His	Phe	Tyr
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Glu

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